

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2003, 10:35:03 ; Search time 85 Seconds
(without alignments)
1251.139 Million cell updates/sec

Title: US-10-057-609B-3
Perfect score: 3448
Sequence: 1 MAAATTTTSSISFSFKP.....IPNGCTFNDVITEGGRIKY 670

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A. Geneseq 19Jun03.*

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 3448 | 100.0 | 670 | 19 | AAW59147 |
| 2 | 3448 | 100.0 | 670 | 22 | AAE02400 |
| 3 | 3443 | 99.9 | 670 | 18 | AAW22457 |
| 4 | 3443 | 99.9 | 670 | 19 | AAW59146 |
| 5 | 3443 | 99.9 | 670 | 21 | AAO54287 |
| 6 | 3442 | 99.8 | 670 | 23 | AAO15640 |
| 7 | 3435 | 99.6 | 670 | 12 | AAO11975 |
| 8 | 3435 | 99.6 | 670 | 13 | AAE26913 |
| 9 | 3435 | 99.6 | 670 | 16 | AAE63082 |
| | | | | | A. thaliana acetol |
| | | | | | Arabidopsis thalia |
| | | | | | Arabidopsis wild-t |
| | | | | | A. thaliana acetol |
| | | | | | Arabidopsis thalia |
| | | | | | Modified Arabidops |
| | | | | | Tobacco herbicide- |
| | | | | | ALS mutant of Arap |
| | | | | | Herbicide-resistan |

| | | | | | | |
|----|--------|------|-----|----|----------|--------------------|
| 10 | 3435 | 99.6 | 670 | 18 | AAW22464 | Arabidopsis herbic |
| 11 | 3425.5 | 99.3 | 669 | 13 | AAE24800 | Ser653 deleted ace |
| 12 | 3422.5 | 99.3 | 669 | 13 | AAE28618 | Ala122 deleted ace |
| 13 | 3422.5 | 99.3 | 669 | 13 | AAE28619 | Ala205 deleted ace |
| 14 | 3422.5 | 99.3 | 669 | 13 | AAE28623 | Val571 deleted ace |
| 15 | 3421.5 | 99.2 | 669 | 13 | AAE28620 | Leu256 deleted ace |
| 16 | 3421.5 | 99.2 | 669 | 13 | AAE28621 | Met351 deleted ace |
| 17 | 3420.5 | 99.2 | 669 | 13 | AAE28617 | Gly121 deleted ace |
| 18 | 3420.5 | 99.2 | 669 | 13 | AAE28622 | Asp376 deleted ace |
| 19 | 3419.5 | 99.2 | 669 | 13 | AAE28624 | Pro197 deleted ace |
| 20 | 3419.5 | 99.2 | 669 | 13 | AAE24799 | Pro197 deleted ace |
| 21 | 3412.5 | 99.0 | 669 | 13 | AAE24798 | Trp574 deleted ace |
| 22 | 3408 | 98.8 | 666 | 13 | AAE28616 | Amino acids 650-65 |
| 23 | 3408 | 98.8 | 668 | 13 | AAE24801 | Pro197/Ser653 dele |
| 24 | 3407.5 | 98.8 | 667 | 13 | AAE28612 | Amino acids 255-25 |
| 25 | 3403 | 98.7 | 666 | 13 | AAE28610 | Amino acids 194-19 |
| 26 | 3402 | 98.7 | 665 | 13 | AAE28609 | Amino acids 119-12 |
| 27 | 3396.5 | 98.5 | 665 | 13 | AAE28614 | Amino acids 373-37 |
| 28 | 3390 | 98.3 | 664 | 13 | AAE28613 | Amino acids 348-35 |
| 29 | 3382 | 98.1 | 662 | 13 | AAE28611 | Amino acids 201-20 |
| 30 | 3364 | 97.6 | 660 | 13 | AAE28615 | Amino acids 569-57 |
| 31 | 2834 | 82.2 | 547 | 21 | AAE54288 | Arabidopsis thalia |
| 32 | 2763.5 | 80.1 | 557 | 9 | AAE81151 | Herbicide resistan |
| 33 | 2685 | 77.9 | 666 | 19 | AAW79141 | Plant acetolactate |
| 34 | 2685 | 77.9 | 666 | 23 | AAE08419 | N. plumbaginifolia |
| 35 | 2683 | 77.8 | 664 | 18 | AAW22455 | Tobacco wild-type |
| 36 | 2671 | 77.5 | 648 | 18 | AAW24473 | Herbicide-sensitiv |
| 37 | 2654.5 | 77.3 | 667 | 18 | AAW22456 | Tobacco wild-type |
| 38 | 2662 | 77.2 | 664 | 17 | AAW00211 | Tobacco hra mutant |
| 39 | 2658.5 | 77.1 | 667 | 12 | AAE11974 | Tobacco SUR-C3 mu |
| 40 | 2658.5 | 77.1 | 667 | 13 | AAE26912 | ALS C3 mutant of t |
| 41 | 2658.5 | 77.1 | 667 | 16 | AAE63081 | ALS SUR-C3 (P197E |
| 42 | 2658.5 | 77.1 | 667 | 17 | AAW00212 | Tobacco C3 mutant |
| 43 | 2658.5 | 77.1 | 667 | 18 | AAW22462 | Tobacco C3 herbici |
| 44 | 2658 | 77.1 | 664 | 9 | AAE81149 | Herbicide resistan |
| 45 | 2657 | 77.1 | 667 | 9 | AAE81150 | Herbicide resistan |

ALIGNMENTS

RESULT 1
AAW59147
ID AAW59147 standard; Protein; 670 AA.

XX AC AAW59147;
XX DT 13-AUG-1998 (first entry)
XX DE A. thaliana acetolactate synthase S653N mutant.
XX DE A. thaliana acetolactate synthase S653N mutant.

KW Acetolactate synthase; ALS; imidazolinone resistance; herbicide; crop;
KW mutant; biosynthesis; valine; leucine; isoleucine; weed removal.

XX OS Arabidopsis thaliana.

XX OS Synthetic.

FX Key Location/Qualifiers
FX FT Modified-site 653
FX FT /label= S653N
FX FT /note= "Wild type Ser is replaced by Asn"

XX XX US5767366-A.

XX XX 16-JUN-1998.

XX XX 22-DEC-1994; 94US-0363208.

XX XX 19-FEB-1991; 91US-0657429.

XX XX 15-DEC-1992; 92US-0990416.

XX XX 22-DEC-1994; 94US-0363208.

XX XX (LOU) UNIV LOUISIANA STATE.

| Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
|--|-------------|---|-----|
| QY | 1 | MAAATTTTSSSISFSTKPSSSSKSPISRSFSLPNSLPNPKSSSSRRRGIKSSSPS | 60 |
| Db | 1 | MAAATTTTSSSISFSTKPSSSSKSPISRSFSLPNSLPNPKSSSSRRRGIKSSSPS | 60 |
| QY | 61 | SISAVLNTNTNTTSPKPKPTETFSRFPADPPKGDILVLEALRQGVETVAYPG | 120 |
| Db | 61 | SISAVLNTNTNTTSPKPKPTETFSRFPADPPKGDILVLEALRQGVETVAYPG | 120 |
| QY | 121 | GASMEIHOALTRSSIRNVLPREHQQGVFAAEGYARSSGKPGICATSGCATNLVSGLA | 180 |
| Db | 121 | GASMEIHOALTRSSIRNVLPREHQQGVFAAEGYARSSGKPGICATSGCATNLVSGLA | 180 |
| QY | 181 | DALLDSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEAPF | 240 |
| Db | 181 | DALLDSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEAPF | 240 |
| QY | 241 | LATSGRPGPVLVDVPKDIQQOLAI PNWQAMLPGYMSRMPKPPEDSHLEQIVRLISESK | 300 |
| Db | 241 | LATSGRPGPVLVDVPKDIQQOLAI PNWQAMLPGYMSRMPKPPEDSHLEQIVRLISESK | 300 |
| QY | 301 | KPVLVYGGGCLNSDELGRFVELTGIPVASTLMGLGYPCCDDELSLHMLGMHGTVYANYA | 360 |
| Db | 301 | KPVLVYGGGCLNSDELGRFVELTGIPVASTLMGLGYPCCDDELSLHMLGMHGTVYANYA | 360 |
| QY | 361 | VHSDLLILAFGRDDEVTGKLEAFASRAKIVHIDIDSABIGKNTPHVSCGVKALQ | 420 |
| Db | 361 | VHSDLLILAFGRDDEVTGKLEAFASRAKIVHIDIDSABIGKNTPHVSCGVKALQ | 420 |
| QY | 421 | GNNKYLENRAELKLDGFWNRELNVQKPFSLFKTFGEAIPPOVAIKVLDLTDGKAI | 480 |
| Db | 421 | GNNKYLENRAELKLDGFWNRELNVQKPFSLFKTFGEAIPPOVAIKVLDLTDGKAI | 480 |
| QY | 481 | ISTGVQGMWAAOFPYNYKPPROWLSSGGLGAMGFLPAAIGASVANPDALVVIDDGGS | 540 |
| Db | 481 | ISTGVQGMWAAOFPYNYKPPROWLSSGGLGAMGFLPAAIGASVANPDALVVIDDGGS | 540 |
| QY | 541 | FIMVQELATIRVENLPVKVLLINNOHLGMWQWEDRFYKANRAHFTLGDPAQDEIFPN | 600 |
| Db | 541 | FIMVQELATIRVENLPVKVLLINNOHLGMWQWEDRFYKANRAHFTLGDPAQDEIFPN | 600 |
| QY | 601 | MLLFAAACGIPPAARVYTKADLREAIQTMLDTPGFLYLDVICPHQEHVLPMPNGSTFNDV | 660 |
| Db | 601 | MLLFAAACGIPPAARVYTKADLREAIQTMLDTPGFLYLDVICPHQEHVLPMPNGSTFNDV | 660 |
| QY | 661 | ITEGDGRIKY 670 | |
| Db | 661 | ITEGDGRIKY 670 | |
| RESULT 3 | | | |
| ID | AAW22457 | standard; Protein; 670 AA. | |
| XX | AC | AAW22457; | |
| DT | 25-MAR-2003 | (updated) | |
| DT | 25-SEP-1997 | (first entry) | |
| XX | DE | Arabidopsis wild-type acetolactate synthase (sub-sequence C). | |
| XX | KW | Acetolactate synthase; ALS; herbicide resistance; transgenic plant; | |
| XX | KW | crop protection. | |
| XX | OS | Arabidopsis thaliana. | |
| XX | XX | Location/Qualifiers | |
| FT | Peptide | 1..90 | |
| FT | Peptide | /label= Transit peptide | |
| FT | Peptide | /note= "putative transit peptide extends for | |
| FT | Peptide | approx. 90 amino acids from N-terminal | |
| FT | Peptide | methionine residue" | |

| | | | |
|---|--------------|---|---------------|
| XX | FN | US5605011-A. | |
| XX | PD | 25-FEB-1997. | |
| XX | PF | 22-DEC-1994; | 94US-0362022. |
| XX | XX | 27-JUL-1987; | 87IL-0083348. |
| PR | 04-MAR-1988; | 88US-0164360. | |
| PR | 18-JAN-1991; | 91US-0642976. | |
| PR | 26-AUG-1986; | 86US-0900609. | |
| PR | 02-JUN-1992; | 92US-0892305. | |
| XX | PA | (DUPO) DU PONT DE NEMOURS & CO E I. | |
| XX | XX | Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR; | |
| PI | Yadav NS; | | |
| XX | XX | WPI; 1997-153232/14. | |
| DR | XX | | |
| XX | XX | | |
| PT | PT | Use of mutant acetolactate synthase genes - for transforming plants | |
| PT | PT | for resistance to sulphonylurea, triazolopyrimidine sulphonamide | |
| XX | XX | and imidazolinone herbicides. | |
| PS | XX | Claim 1; Fig 6a-f; 63pp; English. | |
| XX | CC | Amino acid sub-sequences A-G respectively correspond to the large | |
| CC | CC | subunits of acetolactate synthase (ALS) isozymes I, II and III | |
| CC | CC | (AAW2459-61) from E. coli, and wild-type ALS proteins of yeast | |
| CC | CC | (AAW22458), Arabidopsis thaliana (AAW22457) and tobacco (AAW22455 and | |
| CC | CC | AAW22456). Comparison of these substantially conserved sequences | |
| CC | CC | with those of herbicide-resistant ALS enzymes (see also AA22462-64) | |
| CC | CC | reveals the location of amino acid subunits that lead to herbicide | |
| CC | CC | resistance. In sub-sequence C, such a subunit is located at the | |
| CC | CC | delta-2 position (any amino acid other than alanine). A nucleic | |
| CC | CC | acid encoding an ALS from any source can be mutated so that the | |
| CC | CC | encoded enzyme contains this amino acid subunit. Transformation of | |
| CC | CC | herbicide sensitive plants or plant cells with the nucleic acid | |
| CC | CC | results in resistance to the herbicide. | |
| CC | CC | (Updated on 25-MAR-2003 to correct PF field.) | |
| CC | CC | (Updated on 25-MAR-2003 to correct PR field.) | |
| XX | SQ | Sequence 670 AA; | |
| Query Match 99.9%; Score 3443; DB 18; Length 670; | | | |
| Best Local Similarity 99.9%; Pred. No. 8e-278; 0; Indels 0; Gaps 0; | | | |
| Matches 669; Conservative 1; Mismatches 0; | | | |
| QY | 1 | MAAATTTTSSSISFSTKPSSSSKSPISRSFSLPNSLPNPKSSSSRRRGIKSSSPS | 60 |
| Db | 1 | MAAATTTTSSSISFSTKPSSSSKSPISRSFSLPNSLPNPKSSSSRRRGIKSSSPS | 60 |
| QY | 61 | SISAVLNTNTNTTSPKPKPTETFSRFPADPPKGDILVLEALRQGVETVAYPG | 120 |
| Db | 61 | SISAVLNTNTNTTSPKPKPTETFSRFPADPPKGDILVLEALRQGVETVAYPG | 120 |
| QY | 121 | GASMEIHOALTRSSIRNVLPREHQQGVFAAEGYARSSGKPGICATSGCATNLVSGLA | 180 |
| Db | 121 | GASMEIHOALTRSSIRNVLPREHQQGVFAAEGYARSSGKPGICATSGCATNLVSGLA | 180 |
| QY | 181 | DALLDSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEAPF | 240 |
| Db | 181 | DALLDSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEAPF | 240 |
| QY | 241 | LATSGRPGPVLVDVPKDIQQOLAI PNWQAMLPGYMSRMPKPPEDSHLEQIVRLISESK | 300 |
| Db | 241 | LATSGRPGPVLVDVPKDIQQOLAI PNWQAMLPGYMSRMPKPPEDSHLEQIVRLISESK | 300 |
| QY | 301 | KPVLVYGGGCLNSDELGRFVELTGIPVASTLMGLGYPCCDDELSLHMLGMHGTVYANYA | 360 |
| Db | 301 | KPVLVYGGGCLNSDELGRFVELTGIPVASTLMGLGYPCCDDELSLHMLGMHGTVYANYA | 360 |
| QY | 361 | VHSDLLILAFGRDDEVTGKLEAFASRAKIVHIDIDSABIGKNTPHVSCGVKALQ | 420 |

Db 361 VEHSDDLALAFGRVDFRDRVTGKLEAFASRAKIVHIDIDSABIGKNTKTHVSVCGDVKLALQ 420
 Qy 421 GNNKVLNRAELKLDGVRNENLVOKKPLSKTFGEAIPPOVAIKVLDELTDGKAI 480
 Db 421 GNNKVLNRAELKLDGVRNENLVOKKPLSKTFGEAIPPOVAIKVLDELTDGKAI 480
 Qy 481 ISTGVGQHMAAOFYNNKPRQWLSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
 Db 481 ISTGVGQHMAAOFYNNKPRQWLSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
 Qy 541 FIMNVQELATIRVENLPVKVLLANNOHLGNWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600
 Db 541 FIMNVQELATIRVENLPVKVLLANNOHLGNWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600
 Qy 601 MLFAAACGIPAAARVTKKADLREAIQTMLDTPGYLLDVICPHQEHVLPMPISGTFNDV 660
 Db 601 MLFAAACGIPAAARVTKKADLREAIQTMLDTPGYLLDVICPHQEHVLPMPISGTFNDV 660
 Qy 661 ITEGDEIRIKY 670
 Db 661 ITEGDEIRIKY 670

RESULT 4
 AAG59146 standard; Protein; 670 AA.
 XX AAG59146;
 AC AAM59146;
 DT 13-AUG-1998 (first entry)
 DE A. thaliana acetolactate synthase protein.
 XX Acetolactate synthase; ALS; imidazolinone resistance; herbicide; crop;
 KW mutant; biosynthesis; valine; leucine; isoleucine; weed removal.
 XX Arabidopsis thaliana.

XX US5767366-A.
 XX 16-JUN-1998.
 XX 22-DEC-1994; 94US-0363208.
 XX 19-FEB-1991; 91US-0657429.
 XX 15-DEC-1992; 92US-0990416.
 XX 22-DEC-1994; 94US-0363208.
 XX (LOU) UNIV LOUISIANA STATE.
 XX Murai N, Sathasivan K;
 XX WPI; 1998-361818/31.
 XX N-PSDB; AAV11890.
 XX Imidazolinone resistant mutant aceto:lactate synthase gene - useful
 PT for transforming plants and plant cells to confer resistance to the
 PT herbicide
 XX Disclosure; Page -; 20pp; English.

XX This sequence represents an Arabidopsis thaliana acetolactate
 CC synthase (ALS) protein which is a key enzyme in the biosynthesis of
 CC valine, leucine and isoleucine in plants. This enzyme is inhibited by
 CC herbicides containing imidazolinone e.g. imazapyr, imazazaquin and
 CC imazethapyr. A mutant form of this enzyme, carrying a mutation where a
 CC wild type Ser residue is replaced by an Asn at position 653 results
 CC in an imidazolinone resistant ALS. Transformed plants and cells can be
 CC used to confer imidazolinone resistance on crops, so the herbicide can
 CC be used in the removal of weeds. Current genetic engineering techniques
 CC allow the transfer of the gene to different plant species. Traditional
 CC imidazolinone resistance was only possible by classical breeding

CC techniques, which did not allow trait transfer out of a maize line.
 CC Note: This wild type sequence does not appear in the specification but
 CC has been made from the sequence represented in AAM59146.
 XX
 SQ Sequence 670 AA;
 Query Match 99.9%; Score 3443; DB 19; Length 670;
 Best Local Similarity 99.9%; Pred. No. 8e-278;
 Matches 669; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAATTTTTSSISGFSKPSKSPISFSLPFLSNPKSSSSRRRGIKSSSS 60
 Db 1 MAATTTTTSSISGFSKPSKSPISFSLPFLSNPKSSSSRRRGIKSSSS 60
 Qy 61 SISAVLNTNTNTTTPSTKPTKPTFISFAPDQPRKGADILVEALERQGVETVAYFG 120
 Db 61 SISAVLNTNTNTTTPSTKPTKPTFISFAPDQPRKGADILVEALERQGVETVAYFG 120
 Qy 121 GASMEIHOALTSSSIRNVLPRHOGVFAAGYARSSKSGICGICATSGGANLVSGLA 180
 Db 121 GASMEIHOALTSSSIRNVLPRHOGVFAAGYARSSKSGICGICATSGGANLVSGLA 180
 Qy 181 DALDLSVPLVAITGOVPRRMIGTDAFOETIVEVTRSTKHNLYLMDVDEIPRIIEAFF 240
 Db 181 DALDLSVPLVAITGOVPRRMIGTDAFOETIVEVTRSTKHNLYLMDVDEIPRIIEAFF 240
 Qy 241 LATSGRPGVLVDVPKDIQQOLAI PNWQAMLPQYMSMPKPPEDSHLQIVRLISESK 300
 Db 241 LATSGRPGVLVDVPKDIQQOLAI PNWQAMLPQYMSMPKPPEDSHLQIVRLISESK 300
 Qy 301 KPVLYVGGGLNSDELGRFVELTGIPVASTLMGLSGYPCDDELSLHMLGHGTVVANYA 360
 Db 301 KPVLYVGGGLNSDELGRFVELTGIPVASTLMGLSGYPCDDELSLHMLGHGTVVANYA 360
 Qy 361 VEHSDDLALAFGRVDFRDRVTGKLEAFASRAKIVHIDIDSABIGKNTKTHVSVCGDVKLALQ 420
 Db 361 VEHSDDLALAFGRVDFRDRVTGKLEAFASRAKIVHIDIDSABIGKNTKTHVSVCGDVKLALQ 420
 Qy 421 GNNKVLNRAELKLDGVRNENLVOKKPLSKTFGEAIPPOVAIKVLDELTDGKAI 480
 Db 421 GNNKVLNRAELKLDGVRNENLVOKKPLSKTFGEAIPPOVAIKVLDELTDGKAI 480
 Qy 481 ISTGVGQHMAAOFYNNKPRQWLSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
 Db 481 ISTGVGQHMAAOFYNNKPRQWLSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
 Qy 541 FIMNVQELATIRVENLPVKVLLANNOHLGNWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600
 Db 541 FIMNVQELATIRVENLPVKVLLANNOHLGNWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600
 Qy 601 MLFAAACGIPAAARVTKKADLREAIQTMLDTPGYLLDVICPHQEHVLPMPISGTFNDV 660
 Db 601 MLFAAACGIPAAARVTKKADLREAIQTMLDTPGYLLDVICPHQEHVLPMPISGTFNDV 660
 Qy 661 ITEGDEIRIKY 670
 Db 661 ITEGDEIRIKY 670

RESULT 5
 AAG54287 standard; Protein; 670 AA.
 XX AAG54287;
 AC AAG54287;
 DT 18-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 69201.
 DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX

OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PR 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139849.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.

CC when imidazolinone herbicide is employed using spray over techniques to
CC control weeds within the vicinity. The present amino acid sequence
CC represents a modified version of the Arabidopsis thaliana AHAS protein.
XX
SQ Sequence 670 AA;

Query Match 99.8%; Score 3442; DB 23; Length 670;
Best Local Similarity 99.9%; Pred. No. 9.7e-278;
Matches 669; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAAATTTTSSSISFSTKPSSSSKSPISRSFSLPFSINPNKSSSSRRGKSSSPS 60
Db 1 MAAATTTTSSSISFSTKPSSSSKSPISRSFSLPFSINPNKSSSSRRGKSSSPS 60

Qy 61 SISAVLNTTNTTTPSPKPTKPTFISRFAPDPKRGADILVEALRQGVETVFAYPG 120
Db 61 SISAVLNTTNTTTPSPKPTKPTFISRFAPDPKRGADILVEALRQGVETVFAYPG 120

Qy 121 GASMEIHOALTTRSSIRNVLPREHOGGVFAAEGYARSSGKPGICATSGPGATNLVSGLA 180
Db 121 GASMEIHOALTTRSSIRNVLPREHOGGVFAAEGYARSSGKPGICATSGPGATNLVSGLA 180

Qy 181 DALLDSVPLVAITGOVPRMIGTDAFQETPIVETRSITKHNYLVMVDVPIRIIEAPF 240
Db 181 DALLDSVPLVAITGOVPRMIGTDAFQETPIVETRSITKHNYLVMVDVPIRIIEAPF 240

Qy 241 LATSGRPGVLVDVKDIOQOLAI PNWQAMRLPGYMSRMPKPEDSHLQIVRLISESK 300
Db 241 LATSGRPGVLVDVKDIOQOLAI PNWQAMRLPGYMSRMPKPEDSHLQIVRLISESK 300

Qy 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDELSLHMLGMHGTVYANYA 360
Db 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDELSLHMLGMHGTVYANYA 360

Qy 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDIDSARI GKNTKTPHVSVCDDVKALQ 420
Db 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDIDSARI GKNTKTPHVSVCDDVKALQ 420

Qy 481 ISTGVGQHWAAQFNYNKKPRAWLSSGGLGAMGFGLPAAIGASVANPDVAIWDIDGGS 540
Db 481 ISTGVGQHWAAQFNYNKKPRAWLSSGGLGAMGFGLPAAIGASVANPDVAIWDIDGGS 540

Qy 541 FIMNVOELATIRVENLPVKVLIANNCHLGMWQWEDRFYKANEATFLGDPAQDEIFPN 600
Db 541 FIMNVOELATIRVENLPVKVLIANNCHLGMWQWEDRFYKANEATFLGDPAQDEIFPN 600

Qy 601 MLLFAAACGIPAAVTKKADREAIQTMLDTFGPYLLDVICPHQEHVLFMPNGSTFNDV 660
Db 601 MLLFAAACGIPAAVTKKADREAIQTMLDTFGPYLLDVICPHQEHVLFMPNGSTFNDV 660

Qy 661 ITEGGRIRKY 670
Db 661 ITEGGRIRKY 670

RESULT 7
AAR11975
ID AAR11975 standard; Protein; 670 AA.
XX
AC AAR11975;
XX
DT 25-MAR-2003 (updated)
DT 25-JUL-1991 (first entry)
XX
DE Tobacco herbicide-resistant acetolactate synthase.
XX
KW Tobacco; acetolactate synthase; ALS; herbicide; resistance.
XX
OS Arabidopsis.

XX Key Location/Qualifiers
FH CDS 506..2515
FT /*tag= a
FT /product= ALS
XX
PN US5013659-A.
XX PD 07-MAY-1991.
XX
XX PF 04-MAR-1988; 88US-0164360.
XX PR 04-MAR-1988; 88US-0164360.
XX PR 26-AUG-1986; 86US-0900609.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
XX PI Yadav NS;
XX
XX DR WPI; 1991-156075/21.
XX DR N-PEDB; AAQ11496.
XX
XX PT Nucleic acid fragment - encoding herbicide-resistant plant
XX PT aceto:lactate synthase protein
XX
XX PS Disclosure; Fig 10; 65; English.
XX
XX CC The protein can confer resistance to chloresulfuron up to 30 ppb
XX CC in transformed tobacco calluses.
XX CC See also AAQ11495-6.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 670 AA;

Query Match 99.6%; Score 3435; DB 12; Length 670;
Best Local Similarity 99.7%; Pred. No. 3.7e-277;
Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAAATTTTSSSISFSTKPSSSSKSPISRFSLPFSINPNKSSSSRRGKSSSPS 60
Db 1 MAAATTTTSSSISFSTKPSSSSKSPISRFSLPFSINPNKSSSSRRGKSSSPS 60

Qy 61 SISAVLNTTNTTTPSPKPTKPTFISRFAPDPKRGADILVEALRQGVETVFAYPG 120
Db 61 SISAVLNTTNTTTPSPKPTKPTFISRFAPDPKRGADILVEALRQGVETVFAYPG 120

Qy 121 GASMEIHOALTTRSSIRNVLPREHOGGVFAAEGYARSSGKPGICATSGPGATNLVSGLA 180
Db 121 GASMEIHOALTTRSSIRNVLPREHOGGVFAAEGYARSSGKPGICATSGPGATNLVSGLA 180

Qy 181 DALLDSVPLVAITGOVPRMIGTDAFQETPIVETRSITKHNYLVMVDVPIRIIEAPF 240
Db 181 DALLDSVPLVAITGOVPRMIGTDAFQETPIVETRSITKHNYLVMVDVPIRIIEAPF 240

Qy 241 LATSGRPGVLVDVKDIOQOLAI PNWQAMRLPGYMSRMPKPEDSHLQIVRLISESK 300
Db 241 LATSGRPGVLVDVKDIOQOLAI PNWQAMRLPGYMSRMPKPEDSHLQIVRLISESK 300

Qy 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDELSLHMLGMHGTVYANYA 360
Db 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDELSLHMLGMHGTVYANYA 360

Qy 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDIDSARI GKNTKTPHVSVCDDVKALQ 420
Db 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDIDSARI GKNTKTPHVSVCDDVKALQ 420

Qy 421 GANKVLENRAEELKLD FGVWNEINLVOKKFPISFKTFGAIPPOYAIKVLDELTDGKAI 480
Db 421 GANKVLENRAEELKLD FGVWNEINLVOKKFPISFKTFGAIPPOYAIKVLDELTDGKAI 480

Qy 481 ISTGVGQHWAAQFNYNKKPRAWLSSGGLGAMGFGLPAAIGASVANPDVAIWDIDGGS 540
Db 481 ISTGVGQHWAAQFNYNKKPRAWLSSGGLGAMGFGLPAAIGASVANPDVAIWDIDGGS 540

DB 481 ISTGVGHQWAAQFYNYKPRWMLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
 QY 541 FIMVQELATIRVENLPVKVLLNNHGLGVMQWEDRFYKANRAHTFLGDPQAQDEIFPN 600
 DB 541 FIMVQELATIRVENLPVKVLLNNHGLGVMQWEDRFYKANRAHTFLGDPQAQDEIFPN 600
 QY 601 MLFAAACGIPAAVTKKADLRAIQTMLDTPGYPYLLDVICPHQEHVLPMPNGTNDV 660
 DB 601 MLFAAACGIPAAVTKKADLRAIQTMLDTPGYPYLLDVICPHQEHVLPMPNGTNDV 660
 QY 661 ITEGGRIKY 670
 DB 661 ITEGGRIKY 670

RESULT 8
 AAR26913
 ID AAR26913 standard; Protein; 670 AA.
 XX
 AC AAR26913;
 DT 25-MAR-2003 (updated)
 DT 12-FEB-1993 (first entry)
 XX
 DE ALS mutant of Arabidopsis.
 XX
 KW Herbicide resistant; acetolactate synthase; ALS; sulphonylurea;
 KW triazopyrimidinesulphonamide; imidazolinone; markers.
 OS Arabidopsis thaliana.
 XX
 PN US5141870-A.
 XX
 PD 25-AUG-1992.
 XX
 PF 18-JAN-1991; 91US-0642976.
 XX
 PR 26-AUG-1986; 86US-0900609.
 PR 04-MAR-1988; 88US-0164360.
 PR 18-JAN-1991; 91US-0642976.
 XX
 PA (DUFO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
 PI Yadav NS;
 XX
 DR WPI; 1992-307863/37.
 DR N-FSDS; AAQ26913.
 XX

Conferring herbicide resistance on plants - using a nucleic acid
 fragment encoding a herbicide-resistant plant aceto:lactate
 synthase protein
 XX
 PS Disclosure; Fig 10; 63pp; English.
 XX
 CC The sequence was deduced from a mutant acetolactate synthetase gene
 CC isolated from herbicide resistant strains of Arabidopsis thaliana.
 CC designated GH50. The GH50 mutant ALS gene may be isolated from
 CC Arabidopsis plants resistant to sulphonylurea, triazopyrimidine
 CC sulphonamide and imidazolinone herbicides. The gene may be used to
 CC transform plants to confer herbicide resistance to plants such as
 CC tobacco, pecunia, cotton, sugarbeet, potato, tomato, lettuce,
 CC sunflower, soybean, corn, wheat, rice, poplars, alfalfa, oats, etc.
 CC The herbicide resistant ALS genes can also be used as markers for
 CC transformation of an organism by a second DNA fragment.
 CC See also AAR26911-2.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 670 AA;

Query Match 99.6%; Score 3435; DB 13; Length 670;
 Best Local Similarity 99.7%; Pred. No. 3.7e-277;
 Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAATTTTTSSISFSTKSPSSSKSPILPIGRFSLPFSLPNPKSSSSRRRIGKSSSPS 60
 DB 1 MAATTTTTSSISFSTKSPSSSKSPILPIGRFSLPFSLPNPKSSSSRRRIGKSSSPS 60
 QY 61 SISAVLNTNTNTTTPSTKTPKTFEPIRFPADPFRKADILVEALERQGVETVFAYPG 120
 DB 61 SISAVLNTNTNTTTPSTKTPKTFEPIRFPADPFRKADILVEALERQGVETVFAYPG 120
 QY 121 GASMEHQALTRSSSIRNVLPRIHQGGVPAAGYARSSSKPGICIAISGPGATNLVSGIA 180
 DB 121 GASMEHQALTRSSSIRNVLPRIHQGGVPAAGYARSSSKPGICIAISGPGATNLVSGIA 180
 QY 181 DALDSVPLVAITGVQPRRMIGTDAFOETPIVEVTRSTTKHNYLWMDVEDIPRIIEAPF 240
 DB 181 DALDSVPLVAITGVQPRRMIGTDAFOETPIVEVTRSTTKHNYLWMDVEDIPRIIEAPF 240
 QY 241 LATSGRPGVPLVDVVKDIQQOLATPNWQAMRLPGVMSRMEKPPEDSHLQIVRLISESK 300
 DB 241 LATSGRPGVPLVDVVKDIQQOLATPNWQAMRLPGVMSRMEKPPEDSHLQIVRLISESK 300
 QY 301 KPVLYVGGGCLNSSDELGRFVELTGPVASTLMGLGSGYPCDDLSLHMLGMHGTVYANYA 360
 DB 301 KPVLYVGGGCLNSSDELGRFVELTGPVASTLMGLGSGYPCDDLSLHMLGMHGTVYANYA 360
 QY 361 VEHSDLLAFGRFDDRVTKLEAFASRAKIVHIDIDSAEIGKNTPHVSVCGDVKLAQ 420
 DB 361 VEHSDLLAFGRFDDRVTKLEAFASRAKIVHIDIDSAEIGKNTPHVSVCGDVKLAQ 420
 QY 421 GNMVLENRAEELKLDGFWENELNVOKKFLSPKTFGEAIPPOYAIKVLDELTDGKAI 480
 DB 421 GNMVLENRAEELKLDGFWENELNVOKKFLSPKTFGEAIPPOYAIKVLDELTDGKAI 480
 QY 481 ISTGVGHQWAAQFYNYKPRWMLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
 DB 481 ISTGVGHQWAAQFYNYKPRWMLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
 QY 541 FIMVQELATIRVENLPVKVLLNNHGLGVMQWEDRFYKANRAHTFLGDPQAQDEIFPN 600
 DB 541 FIMVQELATIRVENLPVKVLLNNHGLGVMQWEDRFYKANRAHTFLGDPQAQDEIFPN 600
 QY 601 MLFAAACGIPAAVTKKADLRAIQTMLDTPGYPYLLDVICPHQEHVLPMPNGTNDV 660
 DB 601 MLFAAACGIPAAVTKKADLRAIQTMLDTPGYPYLLDVICPHQEHVLPMPNGTNDV 660
 QY 661 ITEGGRIKY 670
 DB 661 ITEGGRIKY 670

RESULT 9
 AAR63082
 ID AAR63082 standard; Protein; 670 AA.
 XX
 AC AAR63082;
 DT 25-MAR-2003 (updated)
 DT 16-AUG-1995 (first entry)
 XX
 DE Herbicide-resistant ALS (P197A).
 XX
 KW Acetolactate-synthase; ALS; herbicide-resistance; tobacco;
 KW transgenic plant; crop improvement; chlorsulfuron;
 KW sulfometuron methyl; mutagenesis; SURA-C3 gene.
 XX
 OS Arabidopsis thaliana.
 XX
 PN US5378824-A.
 XX
 PD 03-JAN-1995.
 XX
 PF 02-JUN-1992; 92US-0892305.
 XX

PR 27-JUL-1987; 87IL-0083348.
 PR 04-MAR-1988; 88US-0164360.
 PR 18-JAN-1991; 91US-0642976.
 PR 26-AUG-1986; 86US-0900609.
 XX
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Chaleff RS, Yadav NS, Mazur BJ, Falco SC, Somerville CR;
 PI Bedbrook JR;
 XX
 XX
 DR WPI; 1995-065894/09.
 DR N-PSDB; AA081183.
 XX
 PT Nucleic acid fragment encoding a plant aceto:lactate synthase -
 PT confers herbicide resistance when introduced to
 PT herbicide-sensitive plants
 XX
 PS Disclosure; Fig. 10A-10D; 62pp; English.
 XX
 CC Sulfonylurea-resistant mutants of Arabidopsis thaliana were
 CC obtained following ethyl methane sulfonate mutagenesis of seeds.
 CC The mutant acetolactate-synthase (ALS) gene (given in AA081183) was
 CC identified from a genomic DNA library in phage lambda. The
 CC encoded ALS (AAR63082) carried a P197A mutation, leading to improved
 CC resistance to chlorosulfuron and sulfometuron methyl herbicides.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 670 AA;
 Query Match 99.6%; Score 3435; DB 16; Length 670;
 Best Local Similarity 99.7%; Pred. No. 3.7e-277;
 Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAAATTTTSSISFSTKPSSSKSLPISRFSLPFLPNKSSSSRRRGKSSSPS 60
 DB 1 MAAATTTTSSISFSTKPSSSKSLPISRFSLPFLPNKSSSSRRRGKSSSPS 60
 QY 61 SISAVLNTVNTTTPSTKPTPTFISRRAPQPKGADILVLEALRQGVETVAYPG 120
 DB 61 SISAVLNTVNTTTPSTKPTPTFISRRAPQPKGADILVLEALRQGVETVAYPG 120
 QY 121 GASMEIHOALTRSSISRNVLPRHEQGVFAAGVARSKGPGICATSGCATNLVSGLA 180
 DB 121 GASMEIHOALTRSSISRNVLPRHEQGVFAAGVARSKGPGICATSGCATNLVSGLA 180
 QY 181 DALLDSVPLVATGQVPRRMIGTDAFOETPIVEVTRSTKHNVLVMDVEDIPRIIEAFF 240
 DB 181 DALLDSVPLVATGQVPRRMIGTDAFOETPIVEVTRSTKHNVLVMDVEDIPRIIEAFF 240
 QY 241 LATSGRPGVPLVDPKDIOQOLAI PNWEOAMELPGYMRMPKPEDSHLEQIVRLISESK 300
 DB 241 LATSGRPGVPLVDPKDIOQOLAI PNWEOAMELPGYMRMPKPEDSHLEQIVRLISESK 300
 QY 301 KPVLYVGGCLNSDELGRFVELTGIPVASTLMGLSGYPCDDLSLHMLGMHGTVYANYA 360
 DB 301 KPVLYVGGCLNSDELGRFVELTGIPVASTLMGLSGYPCDDLSLHMLGMHGTVYANYA 360
 QY 361 VEHSDLLAFGRFDRVTGKLEAFASRAKIVHIDIDSAEIGKKNKTPHVSVCVDVKALQ 420
 DB 361 VEHSDLLAFGRFDRVTGKLEAFASRAKIVHIDIDSAEIGKKNKTPHVSVCVDVKALQ 420
 QY 421 GNMKVLNFAELKLDLFGWENELNVQKQFPLSKFTFGEAIPPOVAIKVLDELTDGKAI 480
 DB 421 GNMKVLNFAELKLDLFGWENELNVQKQFPLSKFTFGEAIPPOVAIKVLDELTDGKAI 480
 QY 481 ISTGVQCHQWMAAQPTNKKPRONLSSGGLGANGFGLPAATGASVANPDIAVDDIGSGS 540
 DB 481 ISTGVQCHQWMAAQPTNKKPRONLSSGGLGANGFGLPAATGASVANPDIAVDDIGSGS 540
 QY 541 FIMNVOLATIRVENLPVKVLLNNHOLGNWQWEDREYKANAHTFLGDPQAEDEIFPN 600

DB 541 FIMNVOLATIRVENLPVKVLLNNHOLGNWQWEDREYKANAHTFLGDPQAEDEIFPN 600
 QY 601 MLLEFAAACGIPPAARVTKKADLRRAIQTMLDTPGYPYLLDVCIPHOEHLPMIPNGGTFNDV 660
 DB 601 MLLEFAAACGIPPAARVTKKADLRRAIQTMLDTPGYPYLLDVCIPHOEHLPMIPNGGTFNDV 660
 QY 661 ITREGDRIKY 670
 DB 661 ITREGDRIKY 670
 RESULT 10
 AAW22464
 ID AAW22464 standard; Protein; 670 AA.
 XX AC
 AC AAW22464;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-SEP-1997 (first entry)
 XX
 DE Arabidopsis herbicide resistant acetolactate synthase.
 XX
 KW Acetolactate synthase; ALS; herbicide resistance; transgenic plant;
 KW crop protection.
 XX
 OS Arabidopsis thaliana.
 XX
 PN US5605011-A.
 XX
 PD 25-FEB-1997.
 XX
 PF 22-DEC-1994; 94US-0362022.
 XX
 PR 27-JUL-1987; 87IL-0083348.
 PR 04-MAR-1988; 88US-0164360.
 PR 18-JAN-1991; 91US-0642976.
 PR 26-AUG-1986; 86US-0900609.
 PR 02-JUN-1992; 92US-0892305.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
 PI Yadav NS;
 XX
 DR WPI; 1997-153232/14.
 DR N-PSDB; AAT72864.
 XX
 PT Use of mutant acetolactate synthase genes - for transforming plants
 PT for resistance to sulphonylurea, triazoloypyrimidine sulphonamide
 PT and imidazolinone herbicides.
 XX
 PS Disclosure; Fig 10; 63pp; English.
 XX
 CC An Arabidopsis thaliana mutant acetolactate synthases (ALS)
 CC (AAW22463) shows higher resistance to the sulfonylurea herbicides
 CC chlorosulfuron and sulfometuron methyl than the wild-type ALS (see
 CC also AAW22457). The mutant enzyme carries a single Pro to Ser
 CC substn. at the alpha-1 position in comparison to the wild-type
 CC enzyme. A nucleic acid encoding an ALS from any biological source
 CC can be mutated so that the encoded enzyme contains an amino acid
 CC substn. at this position. Transformation of herbicide sensitive
 CC plants or plant cells with the nucleic acid results in resistance
 CC to the herbicide.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 670 AA;
 Query Match 99.6%; Score 3435; DB 18; Length 670;
 Best Local Similarity 99.7%; Pred. No. 3.7e-277;
 Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAAATTTTSSISFSTKPSSSKSLPISRFSLPFLPNKSSSSRRRGKSSSPS 60

RESULT 12

AA28618
ID AAR28618 standard; Protein; 669 AA.

XX AC AAR28618;

XX DT 25-MAR-2003 (updated)
XX DT 11-DEC-1992 (first entry)
XX DE Ala122 deleted acetohydroxy acid synthase.

XX XW AHAS; herbicide resistance; plants; imidazolinones;
XX XW triazolopyrimidines; sulphonylureas.

XX OS Arabidopsis thaliana.

XX PN EP492113-A2.

XX PD 01-JUL-1992.

XX PF 12-NOV-1991; 91EP-0119254.

XX PR 27-DEC-1990; 90US-0633210.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Chaleff RS, Hand JM, Singh BK;

XX DR WPI; 1992-218438/27.

XX DT Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
XX PT nucleic acid sequences which can confer herbicide resistance to
XX PT plants
XX PS Claim 4; Page 20; 37pp; English.

XX CC The sequence is that of Ala122 deleted acetohydroxy acid synthase
XX CC (AHAS) which is herbicide resistant. Transgenic plants may be
XX CC produced which contain the modified gene and produce the Ala122
XX CC Deleted AHAS in the presence of an inhibitory amt. of herbicide.
XX CC The gene can thus be used to provide crop plants with resistance
XX CC to herbicides such as imidazolinones, triazolopyrimidines and
XX CC sulphonylureas. See also AAR24798-R24801 and AAR28609-R28624.
XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 669 AA;

Query Match 99.3%; Score 3422.5; DB 13; Length 669;

Best Local Similarity 99.6%; Pred. No. 4.1e-276;

Matches 667; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAATTTTSSISSTKPSSSSKSLPISRSPLPFSINPNKSSSRGKSSPS 60

DB 1 MAAATTTTSSISSTKPSSSSKSLPISRSPLPFSINPNKSSSRGKSSPS 60

QY 61 SISAVLNTTNTVTTSPKTKPTFFISRPAPQPKGADILVLEALRQGVETVFAYPG 120

DB 61 SISAVLNTTNTVTTSPKTKPTFFISRPAPQPKGADILVLEALRQGVETVFAYPG 120

QY 121 GASMEIHALTRSSINVLPRHQGGVFAAGVARSGRPGICATSGPATNLVSGLA 180

DB 121 G-SMEIHALTRSSINVLPRHQGGVFAAGVARSGRPGICATSGPATNLVSGLA 179

QY 181 DALLDSVPLVAITGOVPRRMIGTDAFOPTTIVETRSITKHNYLVMDVEDIPRIIEAFF 240

DB 180 DALLDSVPLVAITGOVPRRMIGTDAFOPTTIVETRSITKHNYLVMDVEDIPRIIEAFF 239

QY 241 LATSGRPGVLVDYVPKDIQQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300

DB 240 LATSGRPGVLVDYVPKDIQQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 299

QY 301 KPVLYVGGCLNSSLDELGRFVELTGIPVASTMGLGSSYPCCDDELSLHMLGMEGTVYANYA 360
DB 300 KPVLYVGGCLNSSLDELGRFVELTGIPVASTMGLGSSYPCCDDELSLHMLGMEGTVYANYA 359
QY 361 VEHSDLLAFAFGVRRDVRTCKLEAFASRAKIVHIDIDSABEIGKNTKPHVSVCGDVKLALQ 420
DB 360 VEHSDLLAFAFGVRRDVRTCKLEAFASRAKIVHIDIDSABEIGKNTKPHVSVCGDVKLALQ 419
QY 421 GNMKVLNRAEELKLDGFWRNELNVOKKPTLSFKTFGEAIPPOVAIKVLDELTDGKAI 480
DB 420 GNMKVLNRAEELKLDGFWRNELNVOKKPTLSFKTFGEAIPPOVAIKVLDELTDGKAI 479
QY 481 ISTGVQGHQMAAQFYNYKKPROMLSSGGLGAMGFGCPAAIGASVANPDPAIVVDIDGGS 540
DB 480 ISTGVQGHQMAAQFYNYKKPROMLSSGGLGAMGFGCPAAIGASVANPDPAIVVDIDGGS 539
QY 541 FIMNVOELATIRVENLPVKVLLNNOHLGVMWQWEDRFYKANEHTFLGDPAQEDEIFPN 600
DB 540 FIMNVOELATIRVENLPVKVLLNNOHLGVMWQWEDRFYKANEHTFLGDPAQEDEIFPN 599
QY 601 MLLFAAACGIPAAVTKKADIREAIQTMLDTPGYPYLLDVCPHQEHVLPMPINGSTFNDV 660
DB 600 MLLFAAACGIPAAVTKKADIREAIQTMLDTPGYPYLLDVCPHQEHVLPMPINGSTFNDV 659
QY 661 ITEGDGRIKY 670
DB 660 ITEGDGRIKY 669

RESULT 13

AA28619

ID AAR28619 standard; Protein; 669 AA.

XX AC AAR28619;

XX DT 25-MAR-2003 (updated)

XX DT 11-DEC-1992 (first entry)

XX DE Ala205 deleted acetohydroxy acid synthase.

XX XW AHAS; herbicide resistance; plants; imidazolinones;
XX XW triazolopyrimidines; sulphonylureas.
XX OS Arabidopsis thaliana.
XX PN EP492113-A2.
XX PD 01-JUL-1992.

XX PF 12-NOV-1991; 91EP-0119254.

XX PR 27-DEC-1990; 90US-0633210.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Chaleff RS, Hand JM, Singh BK;

XX DR WPI; 1992-218438/27.

XX DT Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
XX PT nucleic acid sequences which can confer herbicide resistance to
XX PT plants
XX PS Claim 4; Page 20; 37pp; English.

XX CC The sequence is that of Ala205 deleted acetohydroxy acid synthase
XX CC (AHAS) which is herbicide resistant. Transgenic plants may be
XX CC produced which contain the modified gene and produce the Ala205
XX CC Deleted AHAS in the presence of an inhibitory amt. of herbicide.
XX CC The gene can thus be used to provide crop plants with resistance
XX CC to herbicides such as imidazolinones, triazolopyrimidines and
XX CC sulphonylureas. See also AAR24798-R24801 and AAR28609-R28624.
XX CC (Updated on 25-MAR-2003 to correct PN field.)

```
XX SQ Sequence 669 AA;
Query Match 99.3%; Score 3422.5; DB 13; Length 669;
Best Local Similarity 99.6%; Pred. No. 4.1e-276;
Matches 667; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAATTTTSSISFSTKPSGSSKSPISRSLSPLFSLPNPKSSSSRRRGIKSSSPS 60
DB 1 MAAATTTTSSISFSTKPSGSSKSPISRSLSPLFSLPNPKSSSSRRRGIKSSSPS 60

QY 61 STSALVNTTNTTTPSPKPKPTETFSRPAPOPRKADILVEALERQGVETVAYPG 120
DB 61 STSALVNTTNTTTPSPKPKPTETFSRPAPOPRKADILVEALERQGVETVAYPG 120

QY 61 STSALVNTTNTTTPSPKPKPTETFSRPAPOPRKADILVEALERQGVETVAYPG 120
DB 61 STSALVNTTNTTTPSPKPKPTETFSRPAPOPRKADILVEALERQGVETVAYPG 120

QY 121 GASMEIHQALTRSSIRNVLPRHEQGGVFAAEGYARSSGKPGICATSGPATNLVSGLA 180
DB 121 GASMEIHQALTRSSIRNVLPRHEQGGVFAAEGYARSSGKPGICATSGPATNLVSGLA 180

QY 181 DALLDSVPLVAITGQVPRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEA 240
DB 181 DALLDSVPLVAITGQVPRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEA 240

QY 241 LATSGRPGPVLVDVPKDIOQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300
DB 241 LATSGRPGPVLVDVPKDIOQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300

QY 301 KPVLYVGGGCLNNSDELGRFVELTGIPVASTLMGLSGYPCCDELSLHMLGMHGTVYANYA 360
DB 301 KPVLYVGGGCLNNSDELGRFVELTGIPVASTLMGLSGYPCCDELSLHMLGMHGTVYANYA 360

QY 361 VHSDDLALAFGRFDRVTGKLEAFASRAKIVHIDIDSABEIGKNTKPHVSVCGDVKLALQ 420
DB 361 VHSDDLALAFGRFDRVTGKLEAFASRAKIVHIDIDSABEIGKNTKPHVSVCGDVKLALQ 420

QY 421 GANKVLENRAEELKLDLFGVWENELNVQKPLSFKTFGEAIPPOYAIKVLDELTDGKAI 480
DB 421 GANKVLENRAEELKLDLFGVWENELNVQKPLSFKTFGEAIPPOYAIKVLDELTDGKAI 480

QY 481 ISTGVGQHWAAQFYNYKKPQWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
DB 481 ISTGVGQHWAAQFYNYKKPQWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540

QY 541 FIMVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGDPAGEDEIFPN 600
DB 541 FIMVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGDPAGEDEIFPN 600
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RESULT 14

AAR28623 standard; Protein; 669 AA.

XX AAR28623;

AC AAR28623;

DT 25-MAR-2003 (updated)

DT 11-DEC-1992 (first entry)

DE Val571 deleted acetohydroxy acid synthase.

XX AHAS; herbicide resistance; plants; imidazolinones;

KW triazolopyrimidines; sulphonylureas.

XX Arabidopsis thaliana.

OS

PN EP492113-A2.

```
XX 01-JUL-1992.
XX 12-NOV-1991; 91EP-0119254.
XX 27-DEC-1990; 90US-0633210.
XX (AMCY) AMERICAN CYANAMID CO.
XX Chaleff RS, Hand JM, Singh BK;
XX WPI; 1992-218438/27.
XX Acetohydroxy acid synthase enzyme deletion mutants - encoded by
XX nucleic acid sequences which can confer herbicide resistance to
XX plants
XX Claim 4; Page 20; 37pp; English.
XX The sequence is that of Val571 deleted acetohydroxy acid synthase
XX (AHAS) which is herbicide resistant. Transgenic plants may be
XX produced which contain the modified gene and produce the Val571
XX deleted AHAS in the presence of an inhibitory amt. of herbicide.
XX The gene can thus be used to provide crop plants with resistance
XX to herbicides such as imidazolinones, triazolopyrimidines and
XX sulphonylureas. See also AAR24798-R24801 and AAR28603-R28624.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 669 AA;
Query Match 99.3%; Score 3422.5; DB 13; Length 669;
Best Local Similarity 99.6%; Pred. No. 4.1e-276;
Matches 667; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAATTTTSSISFSTKPSGSSKSPISRSLSPLFSLPNPKSSSSRRRGIKSSSPS 60
DB 1 MAAATTTTSSISFSTKPSGSSKSPISRSLSPLFSLPNPKSSSSRRRGIKSSSPS 60

QY 61 STSALVNTTNTTTPSPKPKPTETFSRPAPOPRKADILVEALERQGVETVAYPG 120
DB 61 STSALVNTTNTTTPSPKPKPTETFSRPAPOPRKADILVEALERQGVETVAYPG 120

QY 121 GASMEIHQALTRSSIRNVLPRHEQGGVFAAEGYARSSGKPGICATSGPATNLVSGLA 180
DB 121 GASMEIHQALTRSSIRNVLPRHEQGGVFAAEGYARSSGKPGICATSGPATNLVSGLA 180

QY 181 DALLDSVPLVAITGQVPRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEA 240
DB 181 DALLDSVPLVAITGQVPRMIGTDAFOETPIVEVTRSTIKHNYLWMDVEDIPRIIEA 240

QY 241 LATSGRPGPVLVDVPKDIOQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300
DB 241 LATSGRPGPVLVDVPKDIOQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300

QY 301 KPVLYVGGGCLNNSDELGRFVELTGIPVASTLMGLSGYPCCDELSLHMLGMHGTVYANYA 360
DB 301 KPVLYVGGGCLNNSDELGRFVELTGIPVASTLMGLSGYPCCDELSLHMLGMHGTVYANYA 360

QY 361 VHSDDLALAFGRFDRVTGKLEAFASRAKIVHIDIDSABEIGKNTKPHVSVCGDVKLALQ 420
DB 361 VHSDDLALAFGRFDRVTGKLEAFASRAKIVHIDIDSABEIGKNTKPHVSVCGDVKLALQ 420

QY 421 GANKVLENRAEELKLDLFGVWENELNVQKPLSFKTFGEAIPPOYAIKVLDELTDGKAI 480
DB 421 GANKVLENRAEELKLDLFGVWENELNVQKPLSFKTFGEAIPPOYAIKVLDELTDGKAI 480

QY 481 ISTGVGQHWAAQFYNYKKPQWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540
DB 481 ISTGVGQHWAAQFYNYKKPQWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGGS 540

QY 541 FIMVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGDPAGEDEIFPN 600
DB 541 FIMVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGDPAGEDEIFPN 599
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QY 601 MLLFAAACGIPAAAVTKKADLREAIQTMLDTPGYPYLLDVICPHQSHVLPMPNGGTENDV 660
 Db 600 MLLFAAACGIPAAAVTKKADLREAIQTMLDTPGYPYLLDVICPHQSHVLPMPNGGTENDV 659

QY 661 ITEGDGRIKY 670
 Db 660 ITEGDGRIKY 669

RESULT 15
 AAR28620
 ID AAR28620 standard; Protein; 669 AA.
 XX
 AC AAR28620;
 XX
 DT 25-MAR-2003 (updated)
 DT 11-DEC-1992 (first entry)
 XX
 DE Lys256 deleted acetohydroxy acid synthase.
 XX
 XX AHAS; herbicide resistance; plants; imidazolinones;
 KW triazolopyrimidines; sulphonylureas.
 XX
 OS Arabidopsis thaliana.
 XX
 XX EP492113-R2.
 XX
 PD 01-JUL-1992.
 XX
 XX 12-NOV-1991; 91EP-0119254.
 XX
 XX 27-DEC-1990; 90US-0633210.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Chaleff RS, Hand JM, Singh BK;
 XX WPI; 1992-218438/27.
 XX
 XX Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
 FT nucleic acid sequences which can confer herbicide resistance to
 PT plants
 XX
 XX Claim 4; Page 20; 37pp; English.
 XX
 CC The sequence is that of Lys256 deleted acetohydroxy acid synthase
 CC (AHAS) which is herbicide resistant. Transgenic plants may be
 CC produced which contain the modified gene and produce the Lys256
 CC deleted AHAS in the presence of an inhibitory amt. of herbicide.
 CC The gene can thus be used to provide crop plants with resistance
 CC to herbicides such as imidazolinones, triazolopyrimidines and
 CC sulphonylureas. See also AAR24798-R24801 and AAR28609-R28624.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 669 AA;
 SQ

Query March 99.2%; Score 3421.5; DB 13; Length 669;
 Best Local Similarity 99.6%; Pred. No. 5e-276;
 Matches 667; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAATTTTSSISSTKPSKSPISRFSLPFLNPNKSSSSRRRGIKSSSPS 60
 Db 1 MAAATTTTSSISSTKPSKSPISRFSLPFLNPNKSSSSRRRGIKSSSPS 60

QY 61 SISAVLNTTNTTSPKPKDFTFSREAPDQPKGADILVEALRQGVETVFAYPG 120
 Db 61 SISAVLNTTNTTSPKPKDFTFSREAPDQPKGADILVEALRQGVETVFAYPG 120

QY 121 GASMEIHOALTRSSIRNVLPRHEQGVFAAEGYARSSGPKGICATSGPATNLVSGLA 180
 Db 121 GASMEIHOALTRSSIRNVLPRHEQGVFAAEGYARSSGPKGICATSGPATNLVSGLA 180

QY 181 DALLDSVPLVAITGQVPRRMIGTDAFQETPIVETRSITKHNLYLWMDVEDIPRIIEAFF 240
 Db 181 DALLDSVPLVAITGQVPRRMIGTDAFQETPIVETRSITKHNLYLWMDVEDIPRIIEAFF 240

QY 241 LATSGRPGFVLVDPKDIQQOLAI PNWEGAMELPCYMSRMKPPEDSHLEQIVRLISESK 300
 Db 241 LATSGRPGFVLVDVP-DIQQOLAI PNWEGAMELPCYMSRMKPPEDSHLEQIVRLISESK 299

QY 301 KPVLYVGGCLNSDELGRFVELTGIPVASTLMGLSGYPCDDDELSLHMLGMGTYYANYA 360
 Db 300 KPVLYVGGCLNSDELGRFVELTGIPVASTLMGLSGYPCDDDELSLHMLGMGTYYANYA 359

QY 361 VEHSDLLAFGVRFDDRVTKLEAFASRAKIVHIDIISAEI GKNTKPHVSVCGDYKLALQ 420
 Db 360 VEHSDLLAFGVRFDDRVTKLEAFASRAKIVHIDIISAEI GKNTKPHVSVCGDYKLALQ 419

QY 421 GNNKVLNRAEELKIDFGWNRNELNVQKQFPLSFKTFGGEAI PPQYAIKVLDDELTDGKAI 480
 Db 420 GNNKVLNRAEELKIDFGWNRNELNVQKQFPLSFKTFGGEAI PPQYAIKVLDDELTDGKAI 479

QY 481 ISTGVGHOMWAAOFYNYKYPROWLSSGGH GANHGELPAAI GASVANPDALIVDIDGGS 540
 Db 480 ISTGVGHOMWAAOFYNYKYPROWLSSGGH GANHGELPAAI GASVANPDALIVDIDGGS 539

QY 541 FIMNVOELATIRVENLPVKVLLNNQHLGNVWQWEDRFYKANRAHTFLGDPQAQDEIIFPN 600
 Db 540 FIMNVOELATIRVENLPVKVLLNNQHLGNVWQWEDRFYKANRAHTFLGDPQAQDEIIFPN 599

QY 601 MLLFAAACGIPAAAVTKKADLREAIQTMLDTPGYPYLLDVICPHQSHVLPMPNGGTENDV 660
 Db 600 MLLFAAACGIPAAAVTKKADLREAIQTMLDTPGYPYLLDVICPHQSHVLPMPNGGTENDV 659

QY 661 ITEGDGRIKY 670
 Db 660 ITEGDGRIKY 669

Search completed: July 25, 2003, 10:47:12
 Job time : 88 secs

| Result No. | Score | Query | | DB | ID | Description |
|---------------|--------|-------|--------|----|------------------|--------------------|
| | | Match | Length | | | |
| 1 | 3448 | 100.0 | 670 | 1 | US-08-363-208-2 | Sequence 2, Appli |
| 2 | 3448 | 100.0 | 670 | 3 | US-09-137-478-2 | Sequence 2, Appli |
| 3 | 3437.5 | 99.7 | 671 | 2 | US-08-426-125-8 | Sequence 8, Appli |
| 4 | 3437.5 | 99.7 | 671 | 4 | US-08-455-355-8 | Sequence 8, Appli |
| 5 | 3437.5 | 99.7 | 671 | 4 | US-09-367-512-7 | Sequence 7, Appli |
| 6 | 3017 | 87.5 | 652 | 2 | US-08-426-125-9 | Sequence 9, Appli |
| 7 | 3017 | 87.5 | 652 | 2 | US-08-455-355-9 | Sequence 9, Appli |
| 8 | 3017 | 87.5 | 652 | 4 | US-09-367-512-8 | Sequence 8, Appli |
| 9 | 2683 | 77.8 | 664 | 2 | US-08-426-125-7 | Sequence 7, Appli |
| 10 | 2683 | 77.8 | 664 | 2 | US-08-455-355-7 | Sequence 7, Appli |
| 11 | 2683 | 77.8 | 664 | 4 | US-09-367-512-6 | Sequence 6, Appli |
| 12 | 2671 | 77.5 | 648 | 1 | US-08-321-356-4 | Sequence 4, Appli |
| 13 | 2666.5 | 77.3 | 667 | 2 | US-08-426-125-6 | Sequence 6, Appli |
| 14 | 2666.5 | 77.3 | 667 | 2 | US-08-455-355-6 | Sequence 6, Appli |
| 15 | 2666.5 | 77.3 | 667 | 4 | US-09-367-512-5 | Sequence 5, Appli |
| 16 | 2850 | 76.9 | 648 | 1 | US-08-321-356-2 | Sequence 2, Appli |
| 17 | 2611 | 75.7 | 637 | 2 | US-08-426-125-10 | Sequence 10, Appli |
| 18 | 2611 | 75.7 | 637 | 2 | US-08-455-355-10 | Sequence 10, Appli |
| 19 | 2611 | 75.7 | 637 | 4 | US-09-367-512-9 | Sequence 9, Appli |
| 20 | 2348.5 | 68.1 | 638 | 2 | US-08-426-125-5 | Sequence 5, Appli |
| 21 | 2348.5 | 68.1 | 638 | 2 | US-08-455-355-5 | Sequence 5, Appli |
| 22 | 2348.5 | 68.1 | 638 | 4 | US-09-367-512-4 | Sequence 4, Appli |
| 23 | 2338 | 67.8 | 638 | 2 | US-08-426-125-4 | Sequence 4, Appli |
| 24 | 2338 | 67.8 | 638 | 2 | US-08-455-355-4 | Sequence 4, Appli |
| 25 | 2338 | 67.8 | 638 | 4 | US-09-367-512-3 | Sequence 3, Appli |
| 26 | 2334.5 | 67.7 | 599 | 2 | US-08-426-125-3 | Sequence 3, Appli |
| 27 | 2334.5 | 67.7 | 599 | 2 | US-08-455-355-3 | Sequence 3, Appli |

| | | | |
|----|-----|--|-----|
| Db | 1 | MAAATTTTSSSISFSTWPSFSSKSLPIRSFSLPNPNKSSSSRRRGKSSSPS | 60 |
| Qy | 61 | SISAVLNTNTNTTSPKTKPTFFISRPADQPRKGADILVREALRQGVTFVFAYPG | 120 |
| Db | 61 | SISAVLNTNTNTTSPKTKPTFFISRPADQPRKGADILVREALRQGVTFVFAYPG | 120 |
| Qy | 121 | GASMEIHOALTRGSSIRNVLPHEOGGVFAAEGYARSSGKPGICATSGPATNLVUGLA | 180 |
| Db | 121 | GASMEIHOALTRGSSIRNVLPHEOGGVFAAEGYARSSGKPGICATSGPATNLVUGLA | 180 |
| Qy | 181 | DALLDSVPLVAITGOVPRMI GTDAFOPTPIVEVTRSI TKHNYLVMDVEDIPRIIEAFFF | 240 |
| Db | 181 | DALLDSVPLVAITGOVPRMI GTDAFOPTPIVEVTRSI TKHNYLVMDVEDIPRIIEAFFF | 240 |
| Qy | 241 | LATSGRPGVLNDVPKDIQQOLAI PNWEOAMRPGYMSRMPKPPEDSHLEIVELISESK | 300 |
| Db | 241 | LATSGRPGVLNDVPKDIQQOLAI PNWEOAMRPGYMSRMPKPPEDSHLEIVELISESK | 300 |
| Qy | 301 | KPVLYVVGCGCLNSDBELGRFVELTGIPVASTLMGLSYPCCDDELSLHMLGHMGFTVYANYA | 360 |
| Db | 301 | KPVLYVVGCGCLNSDBELGRFVELTGIPVASTLMGLSYPCCDDELSLHMLGHMGFTVYANYA | 360 |
| Qy | 361 | VEHSDLLALFGVDFDRVTGKLEAFASRAKIVHIDDSABEIGNKTPHVSYCGDVKLALQ | 420 |
| Db | 361 | VEHSDLLALFGVDFDRVTGKLEAFASRAKIVHIDDSABEIGNKTPHVSYCGDVKLALQ | 420 |
| Qy | 421 | GNNKVLNRAEBELKLPFGVNRNELNVQKFPPLSFKTFGEAIPPOYAKVLDELTDGKAI | 480 |
| Db | 421 | GNNKVLNRAEBELKLPFGVNRNELNVQKFPPLSFKTFGEAIPPOYAKVLDELTDGKAI | 480 |
| Qy | 481 | I STGVGHQWMAAQFNYNKPKPOMLSSGGLGAMGFGIPAAIGASVANPDALVVIDDGDGS | 540 |
| Db | 481 | I STGVGHQWMAAQFNYNKPKPOMLSSGGLGAMGFGIPAAIGASVANPDALVVIDDGDGS | 540 |
| Qy | 541 | FIMNVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGDPQAQDEIFPN | 600 |
| Db | 541 | FIMNVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGDPQAQDEIFPN | 600 |
| Qy | 601 | MLFAAACGIPAAARVTVKADIREALQTMIDTPGPEYLLDVCPHQEHVLPMPINGGTENDV | 660 |
| Db | 601 | MLFAAACGIPAAARVTVKADIREALQTMIDTPGPEYLLDVCPHQEHVLPMPINGGTENDV | 660 |
| Qy | 661 | ITEGDGRIKY 670 | |
| Db | 661 | ITEGDGRIKY 670 | |

RESULT 2
US-09-137-478-2
; Sequence 2, Application US/09137478
; Patent No. 6225105
; GENERAL INFORMATION:
; APPLICANT: Sathasivan, Kanagasabapathi
; APPLICANT: Murai, No. 6225105imoto
; TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene From
; TITLE OF INVENTION: Arabidopsis Thaliana For Conferring imidazolinone
; TITLE OF INVENTION: Resistance To Crop Plants
; NUMBER OF SEQUENCES: 2

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,429
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Proctor Sr., Llewellyn A.
; REGISTRATION NUMBER: 20,152
; REFERENCE/DOCKET NUMBER: 013911-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (504)275-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 670 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-137-478-2

Query Match 100.0%; Score 3448; DB 3; Length 670;
Best Local Similarity 100.0%; Pred. No. 5e-307;
Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAATATTTTSSGISFSTKPSPPSSSKPLPIGRFSLPSPINPNKSSSSRRRGIKSSSPS 60
Db 1 MAATATTTTSSGISFSTKPSPPSSSKPLPIGRFSLPSPINPNKSSSSRRRGIKSSSPS 60
QY 61 SISAVLNTNTNTVTPSPTKPKPEFIISREAPDOPRGADILVEALERQGVETVFAVPG 120
Db 61 SISAVLNTNTNTVTPSPTKPKPEFIISREAPDOPRGADILVEALERQGVETVFAVPG 120
QY 121 GASMEIHQALTRSSIRNVLPRHEQGVFAARGYARSSKPGICIAATSGCATNLVSGLA 180
Db 121 GASMEIHQALTRSSIRNVLPRHEQGVFAARGYARSSKPGICIAATSGCATNLVSGLA 180
QY 181 DALLDSPVLVAITGVQPRMIGTDACQETPIVEVTSRTTKENYLWMDVEDIPRIIEEAF 240
Db 181 DALLDSPVLVAITGVQPRMIGTDACQETPIVEVTSRTTKENYLWMDVEDIPRIIEEAF 240
QY 241 LATSGRPGPVLVDVPKDIQQQLAIPNWEQAMRLPGYMSRMKPPEDSHLEQIVRLISSEK 300
Db 241 LATSGRPGPVLVDVPKDIQQQLAIPNWEQAMRLPGYMSRMKPPEDSHLEQIVRLISSEK 300
QY 301 KPVLTVGGGCLNSDELGRFVELTGIPVASTLMGLGSPCCDDELSHMLGMGTVYANYA 360
Db 301 KPVLTVGGGCLNSDELGRFVELTGIPVASTLMGLGSPCCDDELSHMLGMGTVYANYA 360
QY 361 VEHSDLLALFAGVRFDDRTVTKLEAFASRAKIVHIDIDSAGIEGKNKTFHVSQGVKLA 420
Db 361 VEHSDLLALFAGVRFDDRTVTKLEAFASRAKIVHIDIDSAGIEGKNKTFHVSQGVKLA 420
QY 421 GKNVKLENRAEELKLDGFGWENELNVOKKPELPSFKTGEAIPPOVAIKVLDLTDGKAI 480
Db 421 GKNVKLENRAEELKLDGFGWENELNVOKKPELPSFKTGEAIPPOVAIKVLDLTDGKAI 480
QY 481 ISTGVGHQHWAAQFYNTKPKRWMLSSGGLGAMGFLPAAIGASVANPDIVVDIDGGS 540
Db 481 ISTGVGHQHWAAQFYNTKPKRWMLSSGGLGAMGFLPAAIGASVANPDIVVDIDGGS 540
QY 541 FIMNVQELATIVENMLPVKVLINNOHLGMWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600
Db 541 FIMNVQELATIVENMLPVKVLINNOHLGMWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600
QY 601 MLFAAAGCIPPAARYTKADIREAIQTMLDTPGPYLLDVI CPQEHVLPMPNGGTFNDV 660
Db 601 MLFAAAGCIPPAARYTKADIREAIQTMLDTPGPYLLDVI CPQEHVLPMPNGGTFNDV 660
QY 661 ITEGDGRIKY 670
Db 661 ITEGDGRIKY 670

```

RESULT 3

US-08-455-355-8

Query Match 99.7%; Score 3437.5; DB 2; Length 671;
Best Local Similarity 99.9%; Pred. No. 4.6e-306;
Matches 670; Conservative 0; Mismatches 0; Indels 1; Caps 1;

QY 1 MAAATTTTSSISFSTKPSKSPKPLPISRFSLPFLSNPNKSSSSRRRGKSSSPS 60
DB 1 MAAATTTTSSISFSTKPSKSPKPLPISRFSLPFLSNPNKSSSSRRRGKSSSPS 60

QY 61 SISAVLNTTNTTTPSTPKTPETFISRPADQPRKGADILVEALERQGVETVAYFG 120
DB 61 SISAVLNTTNTTTPSTPKTPETFISRPADQPRKGADILVEALERQGVETVAYFG 120

QY 121 GASWEIHOALTSSSSIRNVLPRHEOGGVFAAGYARSSGKPGICIAISGPGATNLVSGLA 180
DB 121 GASWEIHOALTSSSSIRNVLPRHEOGGVFAAGYARSSGKPGICIAISGPGATNLVSGLA 180

QY 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKKNYLWMDVEDIPRIIEAPF 240
DB 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKKNYLWMDVEDIPRIIEAPF 240

QY 241 LATSGRPGVPLVDPKIQOOLAI PNWQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300
DB 241 LATSGRPGVPLVDPKIQOOLAI PNWQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300

QY 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCDDLSLHMLGWHGTVYANYA 360
DB 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCDDLSLHMLGWHGTVYANYA 360

QY 361 VEHSDDLALFAGVRFDDRTVTKLEAFASRAKIVHIDIDSABEIGKNKTPHVSVCDDVKLALQ 420
DB 361 VEHSDDLALFAGVRFDDRTVTKLEAFASRAKIVHIDIDSABEIGKNKTPHVSVCDDVKLALQ 420

QY 421 GKNKVLNRABELKLDGFWRNELNVQKFPISFTKFGAIPPOYAIKVLDELTDGKAI 480
DB 421 GKNKVLNRABELKLDGFWRNELNVQKFPISFTKFGAIPPOYAIKVLDELTDGKAI 480

QY 481 ISTGVGQHQAQFNYNKKP-RQWLSGGGIGANGFGLPAAIGASVANPDIAIVDDIDGG 539
DB 481 ISTGVGQHQAQFNYNKKP-RQWLSGGGIGANGFGLPAAIGASVANPDIAIVDDIDGG 540

QY 540 SFIMNVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGPAQOEIIFP 599
DB 540 SFIMNVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGPAQOEIIFP 599

QY 600 NMLLFAAACGIPAAVTKKADLREAIQTMLDTPGYPYLLDVI CPHQEHVLPIMPNGSTFND 659
DB 600 NMLLFAAACGIPAAVTKKADLREAIQTMLDTPGYPYLLDVI CPHQEHVLPIMPNGSTFND 660

QY 660 VITEGDGRIKY 670
DB 661 VITEGDGRIKY 671

RESULT 5

US-09-367-512-7

; Sequence 7, Application US/09367512
; Patent No. 6576455
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; APPLICANT: Kakefuda, Genichi
; APPLICANT: Ott, Karl-Heinz
; APPLICANT: Kwagh, Jae-Gyu
; APPLICANT: Stockton, Gerald W.
; TITLE OF INVENTION: Structure-Based Designed Herbicide Resistant
; FILE REFERENCE: 3489/1A674-US3
; CURRENT APPLICATION NUMBER: US/09/367,512
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 08/426,125
; PRIOR FILING DATE: 1995-04-20
; PRIOR APPLICATION NUMBER: 08/455,355

; PRIOR FILING DATE: 1995-05-31

; PRIOR APPLICATION NUMBER: PCT/US96/05782

; PRIOR FILING DATE: 1996-04-19

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 671

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-367-512-7

Query Match

Best Local Similarity 99.7%; Score 3437.5; DB 4; Length 671;

Matches 670; Conservative 0; Mismatches 0; Indels 1; Caps 1;

QY 1 MAAATTTTSSISFSTKPSKSPKPLPISRFSLPFLSNPNKSSSSRRRGKSSSPS 60

DB 1 MAAATTTTSSISFSTKPSKSPKPLPISRFSLPFLSNPNKSSSSRRRGKSSSPS 60

QY 61 SISAVLNTTNTTTPSTPKTPETFISRPADQPRKGADILVEALERQGVETVAYFG 120

DB 61 SISAVLNTTNTTTPSTPKTPETFISRPADQPRKGADILVEALERQGVETVAYFG 120

QY 121 GASWEIHOALTSSSSIRNVLPRHEOGGVFAAGYARSSGKPGICIAISGPGATNLVSGLA 180

DB 121 GASWEIHOALTSSSSIRNVLPRHEOGGVFAAGYARSSGKPGICIAISGPGATNLVSGLA 180

QY 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKKNYLWMDVEDIPRIIEAPF 240

DB 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKKNYLWMDVEDIPRIIEAPF 240

QY 241 LATSGRPGVPLVDPKIQOOLAI PNWQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300

DB 241 LATSGRPGVPLVDPKIQOOLAI PNWQAMRLPGYMSRMPKPPEDSHLEQIVLISESK 300

QY 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCDDLSLHMLGWHGTVYANYA 360

DB 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCDDLSLHMLGWHGTVYANYA 360

QY 361 VEHSDDLALFAGVRFDDRTVTKLEAFASRAKIVHIDIDSABEIGKNKTPHVSVCDDVKLALQ 420

DB 361 VEHSDDLALFAGVRFDDRTVTKLEAFASRAKIVHIDIDSABEIGKNKTPHVSVCDDVKLALQ 420

QY 421 GKNKVLNRABELKLDGFWRNELNVQKFPISFTKFGAIPPOYAIKVLDELTDGKAI 480

DB 421 GKNKVLNRABELKLDGFWRNELNVQKFPISFTKFGAIPPOYAIKVLDELTDGKAI 480

QY 481 ISTGVGQHQAQFNYNKKP-RQWLSGGGIGANGFGLPAAIGASVANPDIAIVDDIDGG 539

DB 481 ISTGVGQHQAQFNYNKKP-RQWLSGGGIGANGFGLPAAIGASVANPDIAIVDDIDGG 540

QY 540 SFIMNVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGPAQOEIIFP 599

DB 540 SFIMNVQELATIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGPAQOEIIFP 599

QY 600 NMLLFAAACGIPAAVTKKADLREAIQTMLDTPGYPYLLDVI CPHQEHVLPIMPNGSTFND 659

DB 600 NMLLFAAACGIPAAVTKKADLREAIQTMLDTPGYPYLLDVI CPHQEHVLPIMPNGSTFND 660

QY 660 VITEGDGRIKY 670

DB 661 VITEGDGRIKY 671

RESULT 6

US-08-426-125-9

; Sequence 9, Application US/08426125

; Patent No. 5853973

; GENERAL INFORMATION:

; APPLICANT: Kakefuda, Genichi

; APPLICANT: Ott, Karl-Heinz

; APPLICANT: Kwagh, Jae-Gyu

; APPLICANT: Stockton, Gerald W.

;; TITLE OF INVENTION: Structure-Based Designed Herbicide
;; TITLE OF INVENTION: Resistant Products

;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Darby & Darby

;; STREET: 805 Third Avenue

;; CITY: New York

;; STATE: New York

;; COUNTRY: USA

;; ZIP: 10022-7513

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/426,125

;; FILING DATE: 20-APR-1995

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Robinson, Joseph

;; REGISTRATION NUMBER: 33,448

;; REFERENCE/DOCKET NUMBER: 0646/OA674

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (212)-527-7783

;; TELEFAX: (212)-753-6237

;; TELEX: 236687

;; INFORMATION FOR SEQ ID NO: 9:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 652 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; HYPOTHETICAL: NO

;; ORIGINAL SOURCE:

;; ORGANISM: Brassica napus

;; US-08-426-125-9

Query Match 87.5%; Score 3017; DB 2; Length 652;

Best Local Similarity 88.4%; Pred. No. 1.5e-267;

Matches 592; Conservative 29; Mismatches 31; Indels 18; Gaps 4;

QY 1 MAAATTTTSSSISFTKPSSSSKPLPSISRFSPFSLNPNKSSSSRRGIKSSSPS 60

Db 1 MAAA---TSSSPISLTAP---SSKSLPISRESLPSLTQKPSRLR-----PL 46

QY 61 SISAVLNTNTTTPSPKPTKPTFTISRPAQPKGADILVIALERQGVETVFAYPG 120

Db 47 AISAVALSPNVN---APEKTDKI KTFISRYAPDEPRKGADILVIALERQGVETVFAYPG 102

QY 121 GASMEIHOALTRSSIRNVLPRHOGGVFAAEGVARSCKPGICATSPGATNLVSLGA 180

Db 103 GASMEIHOALTRSSIRNVLPRHOGGVFAAEGVARSCKPGICATSPGATNLVSLGA 162

QY 181 DALLDSVPLVAITGOVPRMIGTDAFOETPIVETRSITKHNLYVMDVEDIPRIIEA 240

Db 163 DALLDSVPLVAITGOVPRMIGTDAFOETPIVETRSITKHNLYVMDVDDIPRIVQEAR 222

QY 241 LATSGRPGVLVDPKDIQQOLAIINWEQAMRLPCYMSRMPKPPDSHLEQIVRLISESK 300

Db 223 LATSGRPGVLVDPKDIQQOLAIINWDQPNRLPGYMSRLPQPPVSQLQIVRLISESK 282

QY 301 KPVLYVGGGLNSDELGRFVELTGPVASTLNGLSGPCDDLSLSHMLGHEGTVYANYA 360

Db 283 RVLIVVGGGLNSDELGRFVELTGPVASTLNGLSGPCDDLSLSHMLGHEGTVYANYA 342

QY 361 VEHSDLLIAFGVDFDRVTGKLEAFASRAKIVIHIDDSABEIGKNTKPHVSCGVKLALQ 420

Db 343 VEHSDLLIAFGVDFDRVTGKLEAFASRAKIVIHIDDSABEIGKNTKPHVSCGVKLALQ 402

QY 421 GANKVLENRABELKLDGFWNRNVLNVOQKPLSFKTFTGEAIPPOVAIKVLDLDTQKAI 480

Db 421 GANKVLENRABELKLDGFWNRSELSEQKQKPLSFKTFTGEAIPPOVAIKVLDLDTQKAI 462

QY 481 ISTGVGHQWMAAOFYNYKPRQWLSSGGIGANGRELPAAGASVANPDALVVDIDGGS 540

Db 463 ISTGVGHQWMAAOFYNYKPRQWLSSGGIGANGRELPAAGASVANPDALVVDIDGGS 522

QY 541 FIMVVOELATIRVENLIPVKVLLNNHNLGMVWQWEDRPFYKANRAHTFLGDPACEDRIFPN 600

Db 523 FIMVVOELATIRVENLIPVKVLLNNHNLGMVWQWEDRPFYKANRAHTFLGDPACEDRIFPN 582

QY 601 MLLFAAACGIPPAARVTKKADIREAIQTMLDTGPPYLLVPCPHQEHVLPMPNGGTFNDV 660

Db 583 MLQFAGACGIPPAARVTKKELREAIQTMLDTGPPYLLVPCPHQEHVLPMPNGGTFNDV 642

QY 661 ITEGDGRITKY 670

Db 643 ITEGDGRITKY 652

RESULT 7

US-08-455-355-9

;; Sequence 9, Application US/08455355

;; Patent No. 5928937

;; GENERAL INFORMATION:

;; APPLICANT: Kakefuda, Genichi

;; APPLICANT: Ott, Karl-Heinz

;; APPLICANT: Kwagh, Jae-Gyu

;; APPLICANT: Stockton, Gerald W.

;; TITLE OF INVENTION: Structure-Based Designed Herbicide

;; TITLE OF INVENTION: Resistant Products

;; NUMBER OF SEQUENCES: 10

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Darby & Darby

;; STREET: 805 Third Avenue

;; CITY: New York

;; STATE: New York

;; COUNTRY: USA

;; ZIP: 10022-7513

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/455,355

;; FILING DATE: 31-MAY-1995

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Robinson, Joseph

;; REGISTRATION NUMBER: 33,448

;; REFERENCE/DOCKET NUMBER: 0646/OA674-US1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (212)-527-7783

;; TELEFAX: (212)-753-6237

;; TELEX: 236687

;; INFORMATION FOR SEQ ID NO: 9:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 652 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; HYPOTHETICAL: NO

;; ORIGINAL SOURCE:

;; ORGANISM: Brassica napus

;; US-08-455-355-9

Query Match 87.5%; Score 3017; DB 2; Length 652;

Best Local Similarity 88.4%; Pred. No. 1.5e-267;

Matches 592; Conservative 29; Mismatches 31; Indels 18; Gaps 4;

QY 1 MAAATTTTSSSISFTKPSSSSKPLPSISRFSPFSLNPNKSSSSRRGIKSSSPS 60

Db 1 MAAA---TSSSPISLTAP---SSKSLPISRESLPSLTQKPSRLR-----PL 46

QY 61 SISAVLNTNTTTPSPKPTKPTFTISRPAQPKGADILVIALERQGVETVFAYPG 120

Db 47 AISAVALSPNVN---APEKTDKI KTFISRYAPDEPRKGADILVIALERQGVETVFAYPG 102

QY 121 GASMEIHOALTRSSIRNVLPRHOGGVFAAEGVARSCKPGICATSPGATNLVSLGA 180

Db 103 GASMEIHOALTRSSIRNVLPRHOGGVFAAEGVARSCKPGICATSPGATNLVSLGA 162

COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,125
FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/0A674
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-527-7783
TELEFAX: (212)-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 664 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-426-125-7

Query Match 77.8%; Score 2683; DB 2; Length 664;
Best Local Similarity 76.8%; Pred. No. 6.2e-237;
Matches 523; Conservative 58; Mismatches 72; Indels 28; Gaps 4;

QY 1 MAATTTTSSISFSTKPSKSSKPLPSIFSLPESLNPKNSS-----SSS 49
DB 1 MAATTTTSSISFSTKPSKSSKPLPSIFSLPESLNPKNSS-----SSS 49

QY 50 RRRGKSSPSSISAVLNTTNTTTPSPKTPKTFISRFAPQPKGADILVEALER 109
DB 50 RRRGKSSPSSISAVLNTTNTTTPSPKTPKTFISRFAPQPKGADILVEALER 109

QY 57 RRR-----FTISNVITSTQKSET-----QKAEITVSRFAPDEPKGSDILVEALER 103
DB 57 RRR-----FTISNVITSTQKSET-----QKAEITVSRFAPDEPKGSDILVEALER 103

QY 110 QGVETVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARSSGPGICATSG 169
DB 110 QGVETVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARSSGPGICATSG 169

QY 104 EGVTDVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARATGPGVCATSG 163
DB 104 EGVTDVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARATGPGVCATSG 163

QY 170 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 229
DB 170 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 229

QY 164 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 223
DB 164 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 223

DB 584 NPSNEAIEFPNMLKFAACGVPAARVTHRDDLRRAIQMLTFPGPYLLDVLVPHQHEVLP 643
QY 650 MIPNGGTFNDVITEGDGRIKY 670
DB 644 MIPSGAGFNDVITEGDGRSSY 664

RESULT 10
US-08-455-355-7
Sequence 7, Application US/08455355
Patent No. 5928937
GENERAL INFORMATION:
APPLICANT: Kafefuda, Genichi
APPLICANT: Ott, Karl-Heinz
APPLICANT: Kwagh, Jae-Gyu
APPLICANT: Stockton, Gerald W.
TITLE OF INVENTION: Structure-Based Designed Herbicide
TITLE OF INVENTION: Resistant Products
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dardy & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,355
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A674-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-527-7783
TELEFAX: (212)-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 664 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-355-7

Query Match 77.8%; Score 2683; DB 2; Length 664;
Best Local Similarity 76.8%; Pred. No. 6.2e-237;
Matches 523; Conservative 58; Mismatches 72; Indels 28; Gaps 4;

QY 1 MAATTTTSSISFSTKPSKSSKPLPSIFSLPESLNPKNSS-----SSS 49
DB 1 MAATTTTSSISFSTKPSKSSKPLPSIFSLPESLNPKNSS-----SSS 49

QY 50 RRRGKSSPSSISAVLNTTNTTTPSPKTPKTFISRFAPQPKGADILVEALER 109
DB 50 RRRGKSSPSSISAVLNTTNTTTPSPKTPKTFISRFAPQPKGADILVEALER 109

QY 57 RRR-----FTISNVITSTQKSET-----QKAEITVSRFAPDEPKGSDILVEALER 103
DB 57 RRR-----FTISNVITSTQKSET-----QKAEITVSRFAPDEPKGSDILVEALER 103

QY 110 QGVETVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARSSGPGICATSG 169
DB 110 QGVETVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARSSGPGICATSG 169

QY 104 EGVTDVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARATGPGVCATSG 163
DB 104 EGVTDVAYPGGASMEIHOALTSSSIRNVLPFRHQGGVFAAGYARATGPGVCATSG 163

QY 170 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 229
DB 170 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 229

QY 164 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 223
DB 164 PGATNLVSGIADALLDSVPLVATGQVPRMIGTDAFOETPIVEVTRSTIKHNYLMDVE 223

| | | | | |
|----|---|-----|---|-----|
| QY | | 110 | QGVETVFAYPEGASMEIHOALTSSIRNVLPRIHQGGVFPAAGYARSGKPGICATSGS | 169 |
| | : | | : : | |
| | : | | : : | |
| Db | | 104 | EGVTVDFAYPEGASMEIHOALTSSIRNVLPRIHQGGVFPAAGYARATPGFCIATSG | 163 |
| | : | | : : | |
| | : | | : : | |
| QY | | 170 | PGATNLVSLGLADALLDSVPVAITGOVPRRMIGTDAQETPIVEVTRSTIKHNVLMDVYE | 229 |
| | : | | : : | |
| | : | | : : | |
| Db | | 164 | PGATNLVSLGLADALLDSVPVAITGOVPRRMIGTDAQETPIVEVTRSTIKHNVLMDVYE | 223 |
| | : | | : : | |
| | : | | : : | |
| QY | | 230 | DIPRIIEAFTLATSRGPVLVDVKDIOOOLAPNWQAMELPGYMSRMPKPDPESH | 289 |
| | : | | : : | |
| | : | | : : | |
| Db | | 224 | DIPRVREAFPLARSGRPVLIDVPKDIOOQLVIPWDOPMFLPGYSRSLPKLPENMLL | 283 |
| | : | | : : | |
| | : | | : : | |
| QY | | 290 | EQIVELLISESKPVLAVGGCLNNSDELGRFVELTGTPVASTLMGLGSVCODELSHML | 349 |
| | : | | : : | |
| | : | | : : | |
| Db | | 284 | EQIVELLISESKPVLAVGGCSQSSELRRLVELTGTPVASTLMGLGAFFPGDELSHML | 343 |
| | : | | : : | |
| | : | | : : | |
| QY | | 350 | GMEGTVYANTAVESDLLAAEFGVRFDORVTGKLEAFASRAKIVHIDSABIGKNKTPHY | 409 |
| | : | | : : | |
| Db | | 344 | GMEGTVYANTAVDSSDLLLAGVEFDRDVTGKLEAFASRAKIVHIDSABIGKNKQPHV | 403 |
| | : | | : : | |
| | : | | : : | |
| QY | | 410 | SVCGBVKIALQGANKYLENRABELKLDPGWENELNOKFPLESKFEGALPPOVAIK | 469 |
| | : | | : : | |
| | : | | : : | |
| Db | | 404 | SICADIKIALQGLNSTLSKGKKLUDFGAWOEULTQVKYKPLNFKEFGDALPPOVAIQ | 463 |
| | : | | : : | |
| | : | | : : | |
| QY | | 470 | VILDELTDCGKAISTVGVOHQWAAQFYNYKKCPROWLSGSGELGANGGFLPAAGISVANPD | 529 |
| | : | | : : | |
| | : | | : : | |
| Db | | 464 | VILDELTNGSAISTVGVOHQWAAQYKYRKPROWLTSGGELGANGGFLPAAGAUGRPD | 523 |
| | : | | : : | |
| | : | | : : | |
| QY | | 530 | AIVVIDDGSGFTMNVOELATIRVENLPVKVLLNNQHGMHWOWEDREPYKANAHHTFLG | 589 |
| | : | | : : | |
| | : | | : : | |
| Db | | 524 | EYVVIDDGSGFTMNYOEATIKVENLPVKIMLLNNOHGLGWVYOEWEDREPYKANAHHTYL | 583 |
| | : | | : : | |
| | : | | : : | |
| QY | | 590 | DPAQDEIFFPMILLFAAACGIPPAARVTKKADLRZAIOTMLDTGPGVLIDVICPQEHVLP | 649 |
| | : | | : : | |
| | : | | : : | |
| Db | | 584 | NFSNBAEIFFPMKFLBACCGYPAARVTHRDDLRZAIOKMLDTGPGVLIDVICPQEHVLP | 643 |
| | : | | : : | |
| | : | | : : | |
| QY | | 650 | MIPNGGTENDVITEGDGRIKY | 670 |
| | : | | : : | |
| | : | | : : | |
| Db | | 644 | MIPSGGAFKVITEGDGRSSY | 664 |

RESULT 12
US-08-321-356-4
; Sequence 4, Application US/08321356
; Patent No. 5633437
; GENERAL INFORMATION:
; APPLICANT: Bernasconi, Paul
; APPLICANT: Woodworth, Alison R.
; TITLE OF INVENTION: GENE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: ACETOLACTATE SYNTHASE INHIBITOR HERBICIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SANDOZ AGRO INC.
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk.
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321.356
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marcus-Wyner, Lynn
; REGISTRATION NUMBER: 34869
; REFERENCE/DOCKET NUMBER: 133-0720
; TELECOMMUNICATION INFORMATION:

```

1 COMPUTER: IBM PC COMPACT
2 OPERATING SYSTEM: PC-DOS/MS-DOS
3 SOFTWARE: Patent In Release #1.0, Version #1.25
4
5 CURRENT APPLICATION DATA:
6
7 APPLICATION NUMBER: US/08/321,356
8
9 FILING DATE:
10 CLASSIFICATION: 435
11 ATTORNEY/AGENT INFORMATION:
12
13 NAME: Marcus-Wyner, Lynn
14
15 REGISTRATION NUMBER: 34869
16 REFERENCE/DOCKET NUMBER: 133-0720
17
18 TELECOMMUNICATION INFORMATION:
19

```

TELEPHONE: (415)354-3588
 TELEFAX: (415)857-1125
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 648 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Protein
 US-08-321-356-4

Query Match 77.5%; Score 2671; DB 1; Length 648;
 Best Local Similarity 77.6%; Pred. No. 7.5e-236;
 Matches 521; Conservative 56; Mismatches 70; Indels 24; Gaps 6;

QY 1 MAAATTTTSSISFSTKPSKSPSSKSPSPISFSLPSPKNSSSSSRRRGIKSSPS 60
 DB 1 MAAIPHTNP-----SITTKP-PSPPPTPLAFTPTIT-----STSHKRR-----L 42

QY 61 SIGAVL-NTTNTVTTSTPTKPTPTFISRPAPQPRKADILVEALERQGVETVFAYP 119
 DB 43 HINVLDSKPTIHTSPITK-----SFISRYAPQPRKADILVEALEREGVTDVFAYP 97

QY 120 GGASMEIHOALTRSSIRNVLPRIHQGVFAEGYARSSGKPGICATSPGATNLVSG 179
 DB 98 GGASMEIHOALTRSTIENVLPRHQGVFAEGYARASGLPGVCATSPGATNLVSG 157

QY 180 ADALLDSVPLVAITGVQPRRMIGTDAFOETPIVETVTRSTIKHNLVWVEDIPIIRERAF 239
 DB 158 ADALLDSVPLVAITGVQPRRMIGTDAFOETPIVETVTRSTIKHNLVWVEDIPIIRERAF 217

QY 240 FLATSGRPGVLVDVPKDIQQOLAI PNWQAMLPQYMSRMPKPPEDSHLEQIVRLIS 299
 DB 218 YLASSGRPGVLVDVPKDIQQOLAVPKWDEPIELPGYLSRFPKTNNGQLLEQIVRLVSEA 277

QY 300 KKPVLVGGGLNSDELGRFVELTGIPVASTLMGLSGYPCDDDELSLHMGEGTVIANY 359
 DB 278 KRPVLVGGGLNSGDELRRFVELTGIPVASTLMGLGAYPASSDLSLEMLMGEGTVIANY 337

QY 360 AVESDILLALAFGRVDRVTGKLAFAFASRAKIVHIDISAEIGKKNKPHVSGVDYKAL 419
 DB 338 AVKSULLALAFGRVDRVTGKLAFAFASRAKIVHIDISAEIGKKNKPHVSGVDYKAL 397

QY 420 QGANKVLENABELKIDFGVWRNELNVQKPFLEKFTFGEAIPPOVAIKVLDELDTGKA 479
 DB 398 QGLNKILEKNSVTNLDSNRKELDRQKVKYKPLSEKFTFGEAIPPOVAIQVLDELDTGNA 457

QY 480 IISTGVGQHQWAAOFYNYKPPROWLESGLGAMGFGLPAAGASVANPDIVDDIDGG 539
 DB 458 IISTGVGQHQWAAOFYNYKPPROWLESGLGAMGFGLPAAGASVANPDIVDDIDGG 517

QY 540 SFTMNVQELATIRVENLPVKVLLANNHGLGMWQVEDRKYKANRAHTFLGDPQDEITFP 599
 DB 518 SFTMNVQELATIRVENLPVKVLLANNHGLGMWQVEDRKYKANRAHTFLGDPQDEITFP 577

QY 600 NMLFAAACGIPAAVTKKADLRRAIOTMLDTPGPLYLDVICPHQEHVLPWINGTEND 659
 DB 578 NMLFAEACDIPAAVTEKADLRRAIQKMLDTGPLYLDVICPHQEHVLPWIPAGGFFMD 637

QY 660 VITEGGRMKY 670
 DB 638 VITEGGRMKY 648

RESULT 13
 US-08-426-125-6
 Sequence 6, Application US/08426125
 Patent No. 5853973
 GENERAL INFORMATION:
 APPLICANT: Kafetuda, Genichi
 APPLICANT: Ott, Karl-Heinz
 APPLICANT: Kwagh, Jae-Gyu
 APPLICANT: Stockton, Gerald W.

TITLE OF INVENTION: Structure-Based Designed Herbicide
 TITLE OF INVENTION: Resistant Products
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Darby & Darby
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022-7513
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/426,125
 FILING DATE: 20-APR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Robinson, Joseph
 REGISTRATION NUMBER: 33,448
 REFERENCE/DOCKET NUMBER: 0646/0A674
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)-527-7783
 TELEFAX: (212)-753-6237
 TELEX: 236687
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 667 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 US-08-426-125-6

Query Match 77.3%; Score 2666.5; DB 2; Length 667;
 Best Local Similarity 76.0%; Pred. No. 2e-235;
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QY 1 MAAATTTTSSISFSTKPSKSPSSKSPISRPSLPSLNPKNSS-----S 47
 DB 1 MAAA---APSPSSAPSKTSLSPSSSTSLRPSFPFPHPHKTPPPHLTHTHIH 57

QY 48 SRRRGIKSSPSISAVLNTTNTVTTTPSKPTKETFTISRPAPOPRKADILVEAL 107
 DB 58 SQRRR-----FTISNVISTNOKVSQT-----EKTETFSRPAPOPRKADILVEAL 104

QY 108 ERQGVETVPAYPGGASMEIHOALTRSSIRNVLPRIHQGVFAEGYARSSGKPGICAT 167
 DB 105 ERQGVTDVFPAYPGGASMEIHOALTRSSIRNVLPRIHQGVFAEGYARSGPGVCAT 164

QY 168 SGPGATNLVSGDALDLSVPLVAITGVQPRRMIGTDAFOETPIVETVTRSTIKHNLVMD 227
 DB 165 SGPGATNLVSGDALDLSVPLVAITGVQPRRMIGTDAFOETPIVETVTRSTIKHNLVMD 224

QY 228 VEDIPIIRERAFPLATSGRPGVLVDVPKDIQQOLAI PNWQAMLPQYMSRMPKPPEDS 287
 DB 225 VEDIPIRVREAFPLATSGRPGVLVDVPKDIQQOLAVPKWDEPIELPGYLSRFPKTNNGQLLEQIVRLVSEA 284

QY 288 HLEQIVRLISSEKPKVLYVGGGLNSDELGRFVELTGIPVASTLMGLSGYPCDDDELSD 347
 DB 285 HLEQIVRLISSEKPKVLYVGGGLNSDELGRFVELTGIPVASTLMGLGAFPTGDELSD 344

QY 348 MLGMGTVYANYAVEHSDLLALAFGRVDRVTGKLAFAFASRAKIVHIDISAEIGKKNTP 407
 DB 345 MLGMGTVYANYAVDSSDLLALAFGRVDRVTGKLAFAFASRAKIVHIDISAEIGKKNTP 404

QY 408 HVSVCQDKLALQGNKVLNRAELKLDGFWWRNELNVQKPFLEKFTFGEAIPPOVA 467
 DB 405 HVSICADIKLALQGLNSILSEKGLKLDGFSARQELTEQKVHPLNFKTGDGAIPOVA 464

Search completed: July 25, 2003, 10:51:08
Job time : 33 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2003, 08:16:31 ; Search time 5238 Seconds
(without alignments)
11167.743 Million cell updates/sec

Title: US-10-057-609B-2

Perfect score: 2010

Sequence: 1 atgggggggggaacaacac.....gagatggcgggtaataac 2010

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

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24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hcg_hum.*

31: em_hcg_inv.*

32: em_hcg_other.*

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35: em_hcg_rod.*

36: em_hcg_mam.*

37: em_hcg_vrt.*

38: em_sy.*

39: em_higo_hum.*

40: em_higo_mus.*

41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 2010 | 100.0 | 2365 | 6 | AR148434 |
| 2 | 2010 | 100.0 | 2365 | 8 | ATCSR12 |
| 3 | 2008.4 | 99.9 | 96679 | 8 | ARTSRP19 |
| 4 | 2005.2 | 99.8 | 2263 | 8 | AY042819 |
| 5 | 1978 | 98.4 | 2013 | 8 | AY124092 |
| 6 | 1413.6 | 70.3 | 4724 | 8 | BNHRSYI |
| 7 | 1398.8 | 69.6 | 3386 | 8 | BNHRSYII |
| 8 | 1378.8 | 68.6 | 2019 | 8 | BNHRSYIII |
| 9 | 1345.2 | 66.9 | 1758 | 8 | BNHRSYIV |
| 10 | 1340.2 | 66.7 | 1758 | 8 | RR344986 |
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| 18 | 1316.5 | 65.5 | 1758 | 8 | RR344994 |
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| 21 | 1107 | 55.1 | 2156 | 8 | GHASAS46 |
| 22 | 1106.6 | 55.1 | 2156 | 6 | I44036 |
| 23 | 1106.6 | 55.1 | 2156 | 6 | I44037 |
| 24 | 1106.6 | 55.1 | 2156 | 6 | I44038 |
| 25 | 1106.6 | 55.1 | 2156 | 6 | I44039 |
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| 29 | 1041.6 | 51.8 | 2520 | 6 | I05376 |
| 30 | 1024.4 | 51.0 | 2461 | 6 | NTALSURB |
| 31 | 1018 | 50.6 | 2946 | 6 | I05373 |
| 32 | 1014 | 50.4 | 2065 | 8 | AF363369 |
| 33 | 1009.2 | 50.2 | 2065 | 8 | AF363370 |
| 34 | 1002.6 | 49.9 | 2227 | 8 | AF094326 |
| 35 | 998 | 49.7 | 1703 | 8 | AF308648 |
| 36 | 996.8 | 49.6 | 1968 | 6 | AX367150 |
| 37 | 996.4 | 49.6 | 1703 | 8 | AF308649 |
| 38 | 994.8 | 49.5 | 1703 | 8 | AF308650 |
| 39 | 981.8 | 48.8 | 2208 | 8 | ASUS5852 |
| 40 | 950.6 | 47.3 | 1230 | 8 | RR344995 |
| 41 | 838.2 | 41.7 | 2967 | 6 | I07767 |
| 42 | 837 | 41.6 | 1969 | 8 | I93632 |
| 43 | 837 | 41.6 | 2664 | 8 | ZMAHAS108 |
| 44 | 835.4 | 41.6 | 1969 | 6 | I93633 |
| 45 | 835.4 | 41.6 | 1969 | 6 | I93634 |

ALIGNMENTS

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AR148434
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR148434
Sequence 1
AR148434
AR148434.1
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 2365)
Sathasivan,K. and Murai,N.
Mutant acetolactate synthase gene from Arabidopsis thaliana for
conferring imidazolinone resistance to crop plants
Patent: US 6225105-A 1 01-MAY-2001;

2365 bp
DNA
linear
PAT 08-AUG-2001

1 from patent US 6225105.
GI:15112524


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RESULT 2
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LOCUS ATCS12 2365 bp DNA linear PLN 12-SEP-1993
DEFINITION Arabidopsis thaliana Csr 1.2 gene for acetolactate synthase (BC
4.1.3.18).
ACCESSION X51514.1 GI:16244
VERSION acetolactate synthase; herbicide resistance.
KEYWORDS thale cress. thaliana
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 2365)
AUTHORS Murai, N.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-1990) Murai N., Louisiana State University,
Department of Plant Pathology and Crop Physiology, Baton Rouge, LA
70803, U S A
REFERENCE 2 (bases 1 to 2365)
AUTHORS Sathasivan, K., Haughn, G.W. and Murai, N.
TITLE Nucleotide sequence of a mutant acetolactate synthase gene from an
imidazolinone-resistant Arabidopsis thaliana var. Columbia
JOURNAL Nucleic Acids Res. 18 (8), 2188 (1990)
MEDLINE 90245681
PUBMED 2336405
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variation 2266
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Best local similarity 100.0%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGCGGCAACACACACACACACACATCTTCTTCGATCTCTCTCCACCAACCA 60
Db 309 ATGGCGCGGCAACACACACACACACACATCTTCTTCGATCTCTCTCCACCAACCA 368
QY 61 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 369 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 428
QY 121 AACCCCAACAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

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429 AACCCCAACAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 488
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Db 609 GATATCTCTCTCGAAGCTTTTAGAACCTCAAGCGTAGAACAACCGATTTCCTTACCTTGA 668
QY 361 GGTGATCATATGAGATTCACCAAGCCTTAACCGCTTCTCTCTCAATTCGATTCGATTCCT 420
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Db 909 ATTGGTACAGATGCGTTTCAAGAGACTCCGATTGTTAGGTAACGCGTTCGATTACAGAG 968
QY 661 CATAACTATCTGTGATGATGTTGAAGATATCCCTAGGATTAATGAGGAAGCTTCTTT 720
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QY 721 TRAGTACTCTCTGTAGACCTCGACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 780
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QY 1681 CTTTATTAACCAACAGCATTTGGCATGTTTATGCAATGGAGATCGCTTCTCAAA 1740
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QY 1801 ATGTGCTGTTTGCAGAGCTTGGGATTCAGCGCGAGGCTCACAAGAGAGAGAT 1860
Db 2109 ATGTGCTGTTTGCAGAGCTTGGGATTCAGCGCGAGGCTCACAAGAGAGAGAT 2168
QY 1861 CTCGAGAGCTATTACAGCAATGCTCGATACACAGGACCTTACTGTTGGATGAT 1920
Db 2169 CTCGAGAGCTATTACAGCAATGCTCGATACACAGGACCTTACTGTTGGATGAT 2228
QY 1921 TGTCGCGACCAAGACATGTTGCGGATGATCCGATGATCCGATGATCCGATGATCCGATGATC 1980
Db 2229 TGTCGCGACCAAGACATGTTGCGGATGATCCGATGATCCGATGATCCGATGATCCGATGATC 2288
QY 1981 ATACGGAAGAGATGGCGGATTAATAC 2010
Db 2289 ATACGGAAGAGATGGCGGATTAATAC 2318

RESULT 3

LOCUS AT8P19/c 96679 bp DNA linear PLN 02-DEC-1999
DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T8P19.
ACCESSION AL133315
VERSION AL133315.1 GI:6523080
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 96679)
REFERENCE Choise,N., Robert,C., Brottier,P., Wincker,P., Cattolico,L.,
AUTHORS Artiguenave,F., Saurin,W., Weissenbach,J., Meyers,H.W., Lemcke,K.,
Mayer,K.F.X., Quetier,F. and Salanoubat,M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 96679)

AUTHORS EU Arabidopsis sequencing, project.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mps.biochem.mpg.de, maye@mps.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Grouperment d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Cremieux, BP191, 91006 Evry Cedex, France;
http://www.genoscope.cns.fr
COMMENT Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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 REFERENCE 1 (bases 1 to 2263)
 AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
 Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
 Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
 Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
 Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
 Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
 Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
 Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
 Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
 Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
 Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen, M., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

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 REFERENCE 1 (bases 1 to 2013)
 AUTHORS Jander, G., Baerson, S.R., Hudak, J.A., Gonzalez, K.A., Gruys, K.J. and Last, R.L.
 TITLE Saturation mutagenesis in Arabidopsis to determine frequency of herbicide resistance
 JOURNAL Unpublished
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 AUTHORS Jander, G., Baerson, S.R., Hudak, J.A., Gonzalez, K.A., Gruys, K.J. and Last, R.L.
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 QY 803 AACAGGCTATGAGATTAACCTGTTTATATGCTAGGATGCTTAACTCCCGAAGATTTTC 862
 Db 3266 ATCAACCTATGCTGTTTACCTGCTACATGCTAGGTTGCTCAGGCTCCGGAAGTTCTC 3325
 QY 863 ATTTGAGAGCAGATGTTAGTGTGATTTCTGAGTCTAAGAGCCTGTTGTGTGTTGGTG 922
 Db 3326 AGTTAGTCAAGTCTGTTAGTGTGATTTCTGAGTCTAAGAGCCTGTTGTGTGTTGGTG 3385
 QY 923 GTGCTGTTTGAATCTACGATGAATGAGTGTGTTGTTGAGCTTACGCGGATCCCTG 982
 Db 3386 GTGGAACCTTGAATCTACGATGAAGTGTGTTGAGTGTGTTGAGCTTACGCGGATCCCTG 3445
 QY 983 TTGCGATGATGTTGAGTGTGAGATCTTATCTGTTGATGATGAGTGTGTTGATCA 1042
 Db 3446 TTGCGATGATGTTGAGTGTGAGATCTTATCTGTTGATGATGAGTGTGTTGATCA 3505
 QY 1043 TGCTTGAAGTCAATGAGTGTGATGCAATTAAGCTGCTGAGCATGATGTTGTTGT 1102
 Db 3506 TGCTTGAAGTCAATGAGTGTGATGCAATTAAGCTGCTGAGCATGATGTTGTTGT 3565
 QY 1103 TGGCGTTTGGGTAAGTGTGATGATGCTGCTACGCGTAAAGCTTTCGATGTA 1162
 Db 3566 TGGCGTTTGGTGTGATGATGCTGCTACGCGTAAAGCTTTCGATGTA 3625
 QY 1163 GGGCTAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1222
 Db 3626 GGGCTAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3685
 QY 1223 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1282
 Db 3686 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3745
 QY 1283 ACCGAGCGGAGGCTTAAGCTTGAATTTTGGAGTTTGGAGGATGAGTTGAACGTACAGA 1342

Db 3746 ACCGAGCGGAGGCTCAGCTTCACTTTCGTTTTCGAGGAGTGTGAGGAGCAGA 3805
 QY 1343 AACAGAAGTTTCGTTTCGCTTAAAGACGTTTGGGAAAGTATTCTCCACAGTATGCGA 1402
 Db 3806 AACAGAAGTTTCGTTTCGCTTAAAGACGTTTGGGAAAGTATTCTCCACAGTATGCGA 3865
 QY 1403 TTAAGTCTCTTTCGCTTAAAGACGTTTGGGAAAGTATTCTCCACAGTATGCGA 1462
 Db 3866 TTAAGTCTCTTTCGCTTAAAGACGTTTGGGAAAGTATTCTCCACAGTATGCGA 3925
 QY 1463 ATCAATGTTGGGCGCGCAGTCTTCAATTAACAAACCAAGGAGTGTGCTATCATCAG 1522
 Db 3926 ATCAATGTTGGGCGCGCAGTCTTCAATTAACAAACCAAGGAGTGTGCTATCATCAG 3985
 QY 1523 GAGGCTTGGGAGTATGAGTATTTGGAATTTCTGCTGCGATTTGGAGGCTGTTGCTTAA 1582
 Db 3986 GAGGCTTGGGAGTATGAGTATTTGGAATTTCTGCTGCGATTTGGAGGCTGTTGCTTAA 4045
 QY 1583 CTGATCGGATGTTGCTGATTTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1642
 Db 4046 CTGATCGGATGTTGCTGATTTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 4105
 QY 1643 TAGCCACTATTGCTGTAGAGAACTTTCCAGTGAAGTACTTTTATTATAAACAACAGCAG 1702
 Db 4106 TGCCACATCTCGTGTAGAGAACTTTCCAGTGAAGTACTTTTATTATAAACAACAGCAG 4165
 QY 1703 TTGGCANGTTATGCAATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1762
 Db 4166 TTGGCANGTTATGCAATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 4225
 QY 1763 TCGGGGATCCGGCTCAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1822
 Db 4226 TCGGGGATCCGGCTCAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 4285
 QY 1823 GCGGGATTTCCAGGCGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1882
 Db 4286 GCGGGATTTCCAGGCGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 4345
 QY 1883 TGCTGTGATCAGCAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1942
 Db 4346 TGCTGTGATCAGCAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 4405
 QY 1943 TGCGGATGATCCGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 2002
 Db 4406 TACCGATGATCCGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 4465
 QY 2003 TTAATATAC 2010
 Db 4466 CTAAGTAC 4473

RESULT 7
 BNAHSVIII
 LOCUS B.napus gene for acetohydroxyacid synthase III. 3386 bp DNA linear PLN 17-FEB-1997
 DEFINITION B.napus gene for acetohydroxyacid synthase III.
 ACCESSION Z11526
 VERSION Z11526.1 GI:17775
 KEYWORDS acetohydroxyacid synthase III.
 SOURCE rape.
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 3386)
 AUTHORS Rutledge, R.G., Quillet, T., Hattori, J. and Miki, B.I.
 TITLE Molecular characterization and genetic origin of the *Brassica napus* acetohydroxyacid synthase multigene family
 JOURNAL Mol. Gen. Genet. 229 (1), 31-40 (1991)
 MEDLINE 91375448
 PUBMED 1896019
 REFERENCE 2 (bases 1 to 3386)
 AUTHORS Miki, B.